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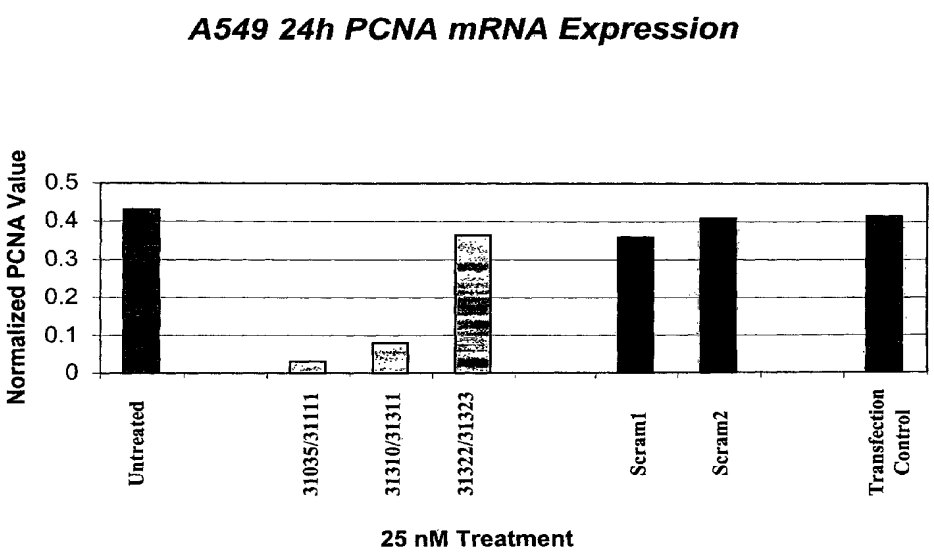
(54) Title: RNA INTERFERENCE MEDIATED INHIBITION OF GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (SINA)



(57) Abstract: The present invention concerns methods and reagents useful in modulating gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against target nucleic acid sequences. The small nucleic acid molecules are useful in the treatment of any disease or condition that responds to modulation of gene expression or activity in a cell, tissue, or organism.

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RNA INTERFERENCE MEDIATED INHIBITION OF GENE EXPRESSION USING SHORT INTERFERING NUCLEIC ACID (siNA)

This invention claims the benefit of Beigelman USSN 60/358,580 filed February 20, 2002, of Beigelman USSN 60/363,124 filed March 11, 2002, of Beigelman USSN 60/386,782 filed June 6, 2002, of Beigelman USSN 60/406,784 filed August 29, 2002, of Beigelman USSN 60/408,378 filed September 5, 2002, of Beigelman USSN 60/409,293 filed September 9, 2002, and of Beigelman USSN 60/440,129 filed January 15, 2003. These applications are hereby incorporated by reference herein in their entireties, including the drawings.

Field Of The Invention

The present invention concerns methods and reagents useful in modulating gene expression in a variety of applications, including use in therapeutic, diagnostic, target validation, and genomic discovery applications. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi).

Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understanding of the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention. Applicant demonstrates herein that chemically modified short interfering nucleic acids possess the same capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity in vivo; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole.

RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.,* 1998, *Nature,* 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an

evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.,* 1999, *Trends Genet.,* 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response though a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein *et al.,* 2001, *Nature,* 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Elbashir *et al.,* 2001, *Genes Dev.,* 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.,* 2001, *Science,* 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.,* 2001, *Genes Dev.,* 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.,* 1998, *Nature,* 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.,* 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.,* 2000, *Nature,* 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.,* 2001, *Nature,* 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in Drosophila embryonic lysates

(Elbashir *et al.,* 2001, *EMBO J.,* 20, 6877) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.,* 2001, *EMBO J.,* 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.,* 2001, *Cell,* 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two -nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.,* 2001, *EMBO J.*, 20, 6877). In addition, Elbashir *et al., supra,* also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li *et al.,* International PCT Publication No. WO 00/44914, and Beach *et al.,* International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge.

However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in siRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1977-1087, tested certain chemical modifications targeting the unc-22 gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified bases also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi system and the use of specific siRNA molecules for certain functional genomic and certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO 00/44914, describe the use of specific dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian

cells using certain dsRNA molecules. Fire *et al.,* International PCT Publication No. WO 99/32619, describe particular methods for introducing certain dsRNA molecules into cells for use in inhibiting gene expression. Plaetinck *et al.,* International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific dsRNA molecules. Mello *et al.,* International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.,* International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents. Waterhouse *et al.,* International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll *et al.,* International PCT Publication No. WO 01/49844, describe specific DNA constructs for use in facilitating gene silencing in targeted organisms.

Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.,* 2000, *Molecular Cell*, 6, 1977-1087, describe specific chemically-modified siRNA constructs targeting the unc-22 gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov *et al.,* International PCT Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.,* International PCT Publication No. WO 01/53475, describe certain methods for isolating a Neurospora silencing gene and uses thereof. Reed *et al.,* International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.,* International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak *et al.,* International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.,* International PCT Publication No. WO 01/92513 describe certain methods for mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.,* International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk *et al.,* International PCT Publication No. WO 00/63364, and Satishchandran *et al.,* International PCT Publication No. WO 01/04313, describe certain

methods and compositions for inhibiting the function of certain polynucleotide sequences using certain dsRNAs. Echeverri *et al.,* International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.,* International PCT Publications Nos. WO 02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using RNAi. Graham *et al.,* International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.,* US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain long dsRNA (greater than 25 nucleotide) constructs that mediate RNAi.

SUMMARY OF THE INVENTION

This invention relates to compounds, compositions, and methods useful for modulating RNA function and/or gene expression in a cell. Specifically, the instant invention features synthetic small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of modulating gene expression in cells by RNA inference (RNAi). The siRNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The use of chemically modified siNA can improve various properties of native siRNA molecules through increased resistance to nuclease degradation *in vivo* and/or improved cellular uptake. The chemically modified siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, agricultural, target validation, genomic discovery, genetic engineering and pharmacogenomic applications.

In a non-limiting example, the introduction of chemically modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given therapeutic effect since chemically modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically modified

nucleic acid molecule is reduced as compared to a native nucleic acid molecule, for example when compared to an all RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siRNA, chemically modified siNA can also minimize the possibility of activating interferon activity in humans.

The siRNA molecules of the invention can be designed to inhibit gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siRNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s). If alternate splicing produces a family of transcipts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siRNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siRNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families. As such, siRNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions

toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in development, such as prenatal development, postnatal development and/or aging.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule that down-regulates expression of a gene family by RNA interference. The gene family can comprise more than one splice variant of a target gene, more than one post-transcriptionally modified RNA of a target gene, or more than one RNA trascript having shared homology. In one embodiment, the gene family comprises epidermal growth factor (e.g., EGFR, such as HER1, HER2, HER3, and/or HER4) genes, vascular endothelial growth factor and vascular endothelial growth factor receptor (e.g., VEGF, VEGFR1, VEGFR2, or VEGFR3) genes, or viral genes corresponding to different viral strains (e.g., HIV-1 and HIV-2). Such gene families can be established by analysing nucleic acid sequences (e.g., sequences shown by Genbank Accession Nos. in **Table V**) for homology.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 21 nucleotides long.

In one embodiment, a siNA molecule of the invention comprises no ribonucleotides. In another embodiment, a siNA molecule of the invention comprises ribonucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of the endogenous mammalian target gene or a portion thereof, and wherein the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence of the endogenous mammalian target gene or a portion thereof.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein each strand of the siNA molecule comprises about 19 to about 23 nucleotides, and wherein each strand comprises about 19 nucleotides that are complementary to the nucleotides of the other strand.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence of the endogenous mammalian target gene or a portion thereof, and wherein the siNA further comprises a sense region, wherein the sense region comprises a nucleotide sequence substantially similar to the nucleotide sequence of the endogenous mammalian target gene or a portion thereof.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the antisense region and the sense region each comprise about 19 to about 23 nucleotides, and wherein the antisense region comprises about 19 nucleotides that are complementary to nucleotides of the sense region.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule comprises a sense region and an antisense region and wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the endogenous mammalian target gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule.

The sense region can be connected to the antisense region via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule comprises a sense region and an antisense region and wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the endogenous mammalian target gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein pyrimidine nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides, 2'-deoxy nucleotides, and/or 2'-deoxy-2'-fluoro pyrimidine nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein the fragment comprising the sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the fragment comprising the sense region. In another embodiment, the terminal cap moiety is an inverted deoxy abasic moiety or glyceryl moiety. In another embodiment, each of the two fragments of the siNA molecule comprise 21 nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule comprises a sense region and an antisense region and wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the endogenous mammalian target gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the purine nucleotides present in the antisense region comprise 2'-deoxy- purine nucleotides. In another embodiment, the antisense region comprises a phosphorothioate

internucleotide linkage at the 3' end of the antisense region. In another embodiment, the antisense region comprises a glyceryl modification at the 3' end of the antisense region.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of an endogenous mammalian target gene (e.g., a human gene), wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule and wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In another embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule are 2'-deoxy-pyrimidines, such as 2'-deoxy-thymidine. In another embodiment, all 21 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the endogenous mammalian target gene. In another embodiment, 21 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the endogenous mammalian target gene. In another embodiment, the 5'-end of the fragment comprising said antisense region optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of an endogenous mammalian target RNA sequence (e.g., wherein said target RNA sequence is encoded by a human gene), wherein the siNA molecule comprises no ribonucleotides and wherein each strand of the double-stranded siNA molecule comprises about 21 nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of an endogenous mammalian target gene (e.g., a human gene such as vascular endothelial growth factor, vascular endothelial growth factor receptor (such as VEGFR1, VEGFR2, or VEGFR3), BCL2, HER2/neu, c-Myc, PCNA, REL-A, PTP1B, BACE, CHK1, PKC-alpha, or EGFR),

wherein the siNA molecule does not require the presence of a ribonucleotide within the siNA molecule for said inhibition of expression of an endogenous mammalian target gene and wherein each strand of the double-stranded siNA molecule is about 21 nucleotides long.

In one embodiment, the invention features a medicament comprising a siNA molecule of the invention.

In one embodiment, the invention features an active ingredient comprising a siNA molecule of the invention.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule to down-regulate expression of an endogenous mammalian target gene, wherein the siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 21 nucleotides long.

In one embodiment, siRNA molecule(s) and/or methods of the invention are used to inhibit the expression of gene(s) that encode RNA referred to by Genbank Accession number in **Table V**. In another embodiment, siRNA molecule(s) and/or methods of the invention are used to target RNA sequence(s) referred to by Genbank Accession number in **Table V**, or nucleic acid sequences encoding such sequences referred to by Genbank Accession number in **Table V**. Such sequences are readily obtained using the Genbank Accession numbers in **Table V**.

In one embodiment, the invention features a siNA molecule having RNAi activity against an RNA encoding a protein, wherein the siNA molecule comprises a sequence complementary to RNA having protein encoding sequence, such as those sequences having GenBank Accession Nos. shown in **Table V**.

In another embodiment, the invention features a siNA molecule having RNAi activity against a gene, wherein the siNA molecule comprises nucleotide sequence complementary to a nucleotide sequence of the gene, such as genes encoding sequences having GenBank Accession Nos. shown in **Table V**. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a gene and thereby mediate silencing of gene expression, for example,

wherein the siNA mediates regulation of gene expression by cellular processes that modulate the chromatin structure of the gene and prevent transcription of the gene.

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence represented by GenBank Accession Nos. shown in **Table V** or a portion of said sequence.

In one embodiment, the nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are chemically modified double stranded nucleic acid molecules. As in their native double stranded RNA counterparts, these siNA molecules typically consist of duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 nucleotides. The most active siRNA molecules are thought to have such duplexes with overhanging ends of 1-3 nucleotides, for example 21 nucleotide duplexes with 19 base pairs and 2 nucleotide 3'-overhangs. These overhanging segments are readily hydrolyzed by endonucleases *in vivo*. Studies have shown that replacing the 3'-overhanging segments of a 21-mer siRNA duplex having 2 nucleotide 3' overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to 4 nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir et al., 2001, EMBO J., 20, 6877). In addition, Elbashir *et al, supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li *et al.,* International PCT Publication No. WO 00/44914, and Beach *et al.,* International PCT Publication No. WO 01/68836 both suggest that siRNA may include modifications to either the phosphate-sugar back bone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however neither application teaches to what extent these modifications are tolerated in siRNA molecules nor provide any examples of such modified siRNA. Kreutzer and Limmer, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double stranded-RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer and Limmer similarly fail to show to what

extent these modifications are tolerated in siRNA molecules nor provide any examples of such modified siRNA.

In one embodiment, the invention features chemically modified siNA constructs having specificity for target nucleic acid molecules in a cell (i.e. target nucleic acid molecules comprising or encoded by seqences referred to herein by Genbank Accession numbers in **Table V**). Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, 2'-deoxy ribonucleotides, "universal base" nucleotides, 5-C-methyl nucleotides, and inverted deoxyabasic residue incorporation. These chemical modifications, when used in various siNA constructs, are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al., supra,* applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA constructs.

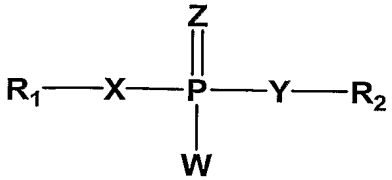
In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise modified nucleotides of about 5 to about 100% of the nucleotide positions (e.g., 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% of the nucleotide positions). The actual percentage of modified nucleotides present in a given siNA molecule depends on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands. In addition, the actual percentage of modified nucleotides present in a given siNA molecule can also depend on the total number of purine and pyrimidine nucleotides present in the siNA, for example wherein all

pyrimidine nucleotides and/or all purine nucleotides present in the siNA molecule are modified.

The antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. The antisense region can comprise about one to about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. The 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. The 3'-terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. The 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding a protein and the sense region can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

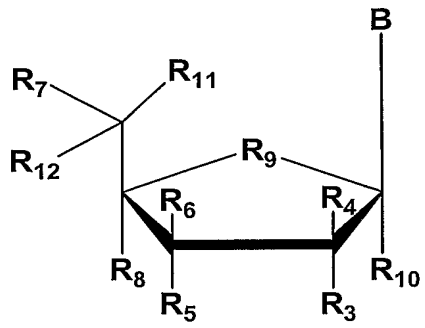
In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:



wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, or aralkyl, and wherein W, X, Y, and Z are optionally not all O.

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide or non-nucleotide having any of Formulae I-VII.

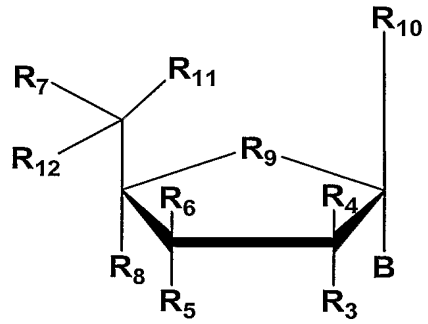
In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula II:



wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In anther non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:



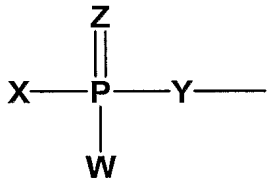
wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-

modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In anther non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or alkylhalo; and wherein W, X, Y and Z are not all O.

In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand, for example, a strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-complementary

strand of a siNA molecule of the invention, for example a siNA molecule having chemical modifications having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a non-limiting example, the invention features a chemically-modified short interfering nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA strands. The phosphorothioate internucleotide linkages can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or

more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3,

4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a

terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

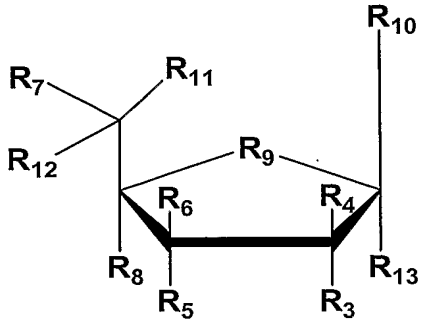
In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45,

46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19 base pairs and 2 loops.

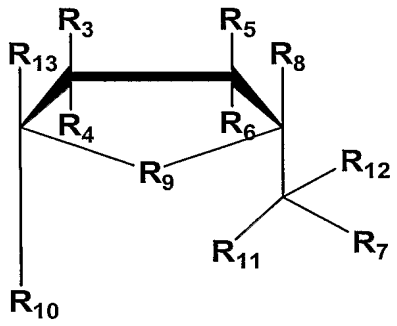
In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2.

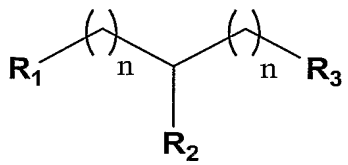
In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or group having Formula I; R9 is O, S, CH2, S=O, CHF, or CF2, and

either R2, R3, R8 or R13 serve as points of attachment to the siNA molecule of the invention.

In another embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) substituted polyalkyl moieties, for example a compound having Formula VII:



wherein each n is independently an integer from 1 to 12, each R1, R2 and R3 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalklylamino, substituted silyl, or a group having Formula I, and R1, R2 or R3 serves as points of attachment to the siNA molecule of the invention.

In another embodiment, the invention features a compound having Formula VII, wherein R1 and R2 are hydroxyl (OH) groups, n = 1, and R3 comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for example modification 6 in **Figure 22**).

In another embodiment, a moiety having any of Formula V, VI or VII of the invention is at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of a siNA molecule of the invention. For example, a moiety having Formula V, VI or VII can be present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense strand, the sense strand, or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises a sense region, where any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine

nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.,* one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.,* one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.,* one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.,* one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention, wherein the chemically-modified siNA comprises an antisense region, where any (*e.g.,* one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and where any (*e.g.,* one or more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are

2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region and an antisense region. The sense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides). Inverted deoxy abasic modifications can be optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region. The sense region optionally further comprises a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides. The antisense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). A terminal cap modification, such as any modification described herein or shown in **Figure 22**, is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The antisense region optionally further comprises a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 18 and 19** and **Table IV** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the siNA comprises a sense region and an antisense region, wherein the sense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-

fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine ribonucleotides (e.g., wherein all purine nucleotides are purine ribonucleotides or alternately a plurality of purine nucleotides are purine ribonucleotides) and wherein the antisense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Inverted deoxy abasic modifications are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region. The sense region optionally further comprises a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides. A terminal cap modification, such as any modification described herein or shown in **Figure 22**, is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The antisense region optionally further comprises a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 18 and 19** and **Table IV** herein.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemically-modified siNA comprises a sense region and an antisense region, wherein the sense region comprises one or 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (*e.g.*, wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately

a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides) and wherein the antisense region comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides). Inverted deoxy abasic modifications are optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense region. The sense region optionally further comprises a 3'-terminal overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxyribonucleotides. A terminal cap modification, such as any modification described herein or shown in **Figure 22**, is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The antisense region optionally further comprises a 3'-terminal nucleotide overhang having about 1 to about 4 (e.g., about 1, 2, 3, or 4) 2'-deoxynucleotides, wherein the overhang nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages.

In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also

optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2′-O,4′-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule. In another embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule into a biological system, such as a cell. In another embodiment, the conjugate molecule attached to the chemically-modified siNA molecule is a poly ethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.,* U.S. Serial No. 10/201,394, incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified with various conjugates to determine whether the siNA conjugate complex possesses improved properties while

maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of ≥ 2 nucleotides in length, for example 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.,* 1995, *Annu. Rev. Biochem.,* 64, 763; Brody and Gold, 2000, *J. Biotechnol.,* 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.,* 2, 100; Kusser, 2000, *J. Biotechnol.,* 74, 27; Hermann and Patel, 2000, *Science,* 287, 820; and Jayasena, 1999, *Clinical Chemistry,* 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, *18*:6353 and *Nucleic Acids Res.* 1987, *15*:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, *113*:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, *113*:5109; Ma *et al., Nucleic Acids Res.* 1993, *21*:2585 and *Biochemistry* 1993, *32*:1751; Durand *et al., Nucleic Acids Res.* 1990, *18*:6353; McCurdy *et al., Nucleosides & Nucleotides* 1991, *10*:287; Jschke *et al., Tetrahedron Lett.* 1993, *34*:301; Ono *et al., Biochemistry* 1991, *30*:9914; Arnold *et al.,* International Publication No. WO 89/02439; Usman *et al.,* International Publication No.

WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, *113*:4000, all hereby incorporated by reference herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. For example, a siNA molecule can be assembled from a single oligonculeotide where the sense and antisense regions of the siNA comprise separate oligonucleotides not having any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotides. In another example, a siNA molecule can be assembled from a single oligonculeotide where the sense and antisense regions of the siNA are linked or circularized by a nucleotide or non-nucleotide linker as desrcibed herein, wherein the oligonucleotide does not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotide. Applicant has surprisingly found that the presense of ribonucleotides (e.g., nucleotides having a 2'-hydroxyl group) within the siNA molecule is not required or essential to support RNAi activity. As such, in one embodiment, all positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal

phosphate group and a 3'-terminal phosphate group (e.g., a 2', 3'-cyclic phosphate). In another embodiment, the single stranded siNA molecule of the invention comprises about 19 to about 29 nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 22**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any

purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 22**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine nucleotides are LNA nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 22**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system, wherein the siNA molecule comprises a single stranded polynucleotide having complementarity to a target nucleic acid sequence, and wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine

nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 22**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence, the siNA optionally further comprising about 1 to about 4 (e.g., about 1, 2, 3, or 4) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, or 4) phosphorothioate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group.

In another embodiment, any modified nucleotides present in the single stranded siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

In one embodiment, the invention features a method for modulating the expression of a gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the gene in the cell.

In one embodiment, the invention features a method for modulating the expression of a gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene and wherein the sense strand sequence of the siNA comprises a sequence substantially similar to the sequence of the target RNA;

and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the genes; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the genes in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene and wherein the sense strand sequence of the siNA comprises a sequence substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the genes in the cell.

In one embodiment, siNA molecules of the invention are used as reagents in ex vivo applications. For example, siNA reagents are intoduced into tissue or cells that are transplanted into a subject for therapeutic effect. The cells and/or tissue can be derived from an organism or subject that later receives the explant, or can be derived from another organism or subject prior to transplantation. The siNA molecules can be used to modulate the expression of one or more genes in the cells or tissue, such that the cells or tissue obtain a desired phenotype or are able to perform a function when transplanted in vivo. In one embodiment, certain target cells from a patient are extracted. These extracted cells are contacted with siNAs targeteing a specific nucleotide sequence within the cells under conditions suitable for uptake of the siNAs by these cells (e.g. using delivery reagents such as cationic lipids, liposomes and the like or using techniques such as electroporation to facilitate the delivery of siNAs into cells). The cells are then reintroduced back into the same patient or other patients. Non-limiting examples of ex vivo applications include use in organ/tissue transplant, tissue grafting, or treatment of pulmonary disease (e.g., restenosis) or prevent neointimal hyperplasia and atherosclerosis in vein grafts. Such ex vivo applications may also used to treat conditions associated with

coronary and peripheral bypass graft failure, for example, such methods can be used in conjunction with peripheral vascular bypass graft surgery and coronary artery bypass graft surgery. Additional applications include transplants to treat CNS lesions or injury, including use in treatment of neurodegenerative conditions such as Alzheimer's disease, Parkinson's Disease, Epilepsy, Dementia, Huntington's disease, or amyotrophic lateral sclerosis (ALS).

In one embodiment, the invention features a method of modulating the expression of a gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the gene in that organism.

In one embodiment, the invention features a method of modulating the expression of a gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene and wherein the sense strand sequence of the siNA comprises a sequence substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the genes; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism

under conditions suitable to modulate the expression of the genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the genes in the organism.

In one embodiment, the invention features a method for modulating the expression of a gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) contacting the siNA molecule with a cell in vitro or in vivo under conditions suitable to modulate the expression of the genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the

invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) contacting the siNA molecule with a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the gene; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a gene in an organism comprising contacting the organism with a siNA molecule of the

invention under conditions suitable to modulate the expression of the gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one gene in an organism comprising contacting the organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the genes in the organism.

The siNA molecules of the invention can be designed to inhibit target gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families. As such, siNA molecules targeting multiple gene targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of

target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, in development, such as prenatal development and postnatal development, and/or the progression and/or maintenance of cancer, infectious disease, autoimmunity, inflammation, endocrine disorders, renal disease, pulmonary disease, cardiovascular disease, birth defects, ageing, any other disease or condition related to gene expression.

In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNAse protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4^N, where N represents the number of base paired nucleotides in each of the siNA construct strands (*eg.* for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be 4^{19}); and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA

molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 7 herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNAse protection assays, to determine the most suitable target site(s) within the target RNA sequence. In another embodiment, the target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNAse protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the

background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a method for treating or preventing a disease or condition in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other therapeutic compounds. In yet another embodiment, the invention features a method for reducing or preventing tissue rejection in a subject comprising administering to the subject a composition of the invention under conditions suitable for the reduction or prevention of tissue rejection in the subject.

In another embodiment, the invention features a method for validating a gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the target gene in the cell, tissue, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

In another embodiment, the invention features a method for validating a target gene comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

By "biological system" is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human, animal, plant, insect, bacterial, viral or other sources, wherein the system comprises the components required for RNAi acitivity. The term "biological system" includes, for example, a cell, tissue, or organism, or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a target gene in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one target gene in a cell, tissue, or organism.

In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a target gene in a biological system. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one target gene in a biological system.

In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide synthesis. In yet another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety than can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an

oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

In one embodiment, the invention features siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of Formulae I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

In one embodiment, the invention features siNA constructs that mediate RNAi against a target gene, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of

step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

In one embodiment, the invention features siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

In one embodiment, the invention features siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

In one embodiment, the invention features siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the siNA construct comprises one or more chemical modifications described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA molecule.

In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the chemical modifications do not significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity, comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a target RNA comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a DNA target comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the DNA target, such as a gene, chromosome, or portion thereof.

In one embodiment, the invention features siNA constructs that mediate RNAi in a cell or reconstituted system, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules against a target gene with improved cellular uptake comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

In one embodiment, the invention features siNA constructs that mediate RNAi against a target gene, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such conjugates are described in Vargeese *et al.*, U.S. Serial No. 10/201,394 incorporated by reference herein.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability, comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as polyethyleneglycol (PEG); phospholipids; polyamines, such as spermine or spermidine; and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 2,000 to about 50,000 daltons (Da).

The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include a siNA molecule of the invention and a vehicle that promotes introduction of the siNA into cells of interest as described herein (e.g., using lipids and other methods of transfection known in the art, see for example Beigelman *et al,* US 6,395,713). The kit can be used for target validation, such as in determining gene function and/or activity, or in drug optimization, and in drug discovery (see for example Usman et al., USSN 60/402,996). Such a kit can also include instructions to allow a user of the kit to practice the invention.

The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication, for example by mediating RNA interference "RNAi" or gene silencing in a sequence-specific manner; see for example Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.,* 2001, *Nature*, 411, 494-498; and Kreutzer *et al.,* International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.,* International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.,* International PCT Publication No. WO 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.,* International PCT Publication No. WO 00/44914; Allshire, 2002, *Science,* 297, 1818-1819; Volpe *et al.,* 2002, *Science,* 297, 1833-1837; Jenuwein, 2002, *Science,* 297, 2215-2218; and Hall *et al.,* 2002, *Science,* 297, 2232-2237;

Hutvagner and Zamore, 2002, *Science*, 297, 2056-60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non limiting examples of siNA molecules of the invention are shown in **Figures 4-6,** and **Tables II, III, and IV** herein. For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 19 base pairs); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo* or *in vitro* to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide

sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell.*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiment, the siNA molecule of the invention comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linkers molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der waals interactions, hydrophobic intercations, and/or stacking interactions. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified

oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Allshire, 2002, *Science,* 297, 1818-1819; Volpe *et al.,* 2002, *Science,* 297, 1833-1837; Jenuwein, 2002, *Science,* 297, 2215-2218; and Hall *et al.,* 2002, *Science,* 297, 2232-2237).

By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

By "inhibit" it is meant that the activity of a gene expression product or level of RNAs or equivalent RNAs encoding one or more gene products is reduced below that observed in the absence of the nucleic acid molecule of the invention. In one embodiment, inhibition with a siNA molecule preferably is below that level observed in the presence of an inactive or attenuated molecule that is unable to mediate an RNAi response. In another embodiment, inhibition of gene expression with the siNA molecule of the instant invention is greater in the presence of the siNA molecule than in its absence.

By "inhibit", "down-regulate", or "reduce", it is meant that the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, is reduced below that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In one embodiment, inhibition, down-regulation or reduction with an siNA molecule is below that level observed in the presence of an inactive or attenuated molecule. In another embodiment, inhibition, down-regulation, or reduction with siNA

molecules is below that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment, inhibition, down-regulation, or reduction of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence.

By "gene" or "target gene" is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts.

By "endogenous" or "cellular" gene is meant a gene normally found in a cell in its natural location in the genome. For example, HER-2, VEGF, VEGF-R, EGFR, BCL-2, c-MYC, RAS and the like would be considered an endogenous gene. Genes expressed in a cell from a plasmid, viral vector or other vectors or from virus, bacteria, fungi would be considered "foreign" or "heterologous" gene; such genes are not normally found in the host cell, but are introduced by standard gene transfer techniques or as a result of infection by a virus, bacterial or other infectious agent.

By "gene family" is meant a group of more than one nucleic acid molecules that share at least one common characteristic, such as sequence homology, target specificity, mode of action, secondary structure, or the ability to modulate a process or more than one process in a biological system. The gene family can be of viral or cellular origin. The gene family can encode, for example, groups of cytokines, receptors, growth factors, adapter proteins, structural proteins, and other protein epitopes.

By "protein family" is meant a group of more than one proteins, peptides, or polypeptides that share at least one common characteristic, such as sequence homology, target specificity, mode of action, secondary structure, or the ability to modulate a process or more than one process in a biological system. The protein family can be of viral or

cellular origin. The protein family can encode, for example, groups of cytokines, receptors, growth factors, adapter proteins, structural proteins, and other protein epitopes.

By "highly conserved sequence region" is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

By "cancer" is meant a group of diseases characterized by uncontrolled growth and spread of abnormal cells.

By "sense region" is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By "antisense region" is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

By "target nucleic acid" is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.,* 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.,* 1986, *Proc. Nat. Acad. Sci.* USA 83:9373-9377; Turner *et al.,* 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous

residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

The siNA molecules of the invention represent a novel therapeutic approach to a broad spectrum of diseases and conditions, including cancer or cancerous disease, infectious disease, cardiovascular disease, neurological disease, prion disease, inflammatory disease, autoimmune disease, pulmonary disease, renal disease, liver disease, mitochondrial disease, endocrine disease, reproduction related diseases and conditions, and any other indications that can respond to the level of an expressed gene product in a cell or organsim.

In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to about 23 base pairs (*e.g.*, about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment, siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (*e.g.*, about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44 (*e.g.*, 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (*e.g.*, about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Table II**. Exemplary synthetic siNA molecules of the invention are shown in **Table I** and/or **Figures 18-19**.

As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell can be present in an organism, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or

without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables I-II** and/or **Figures 18-19**. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in **Table IV** can be applied to any siNA sequence of the invention.

In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β-D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. In one embodiment, a subject is a mammal or mammalian cells. In another embodiment, a subject is a human or human cells.

The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art (see for example Loakes, 2001, *Nucleic Acids Research,* 29, 2437-2447).

The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein. For example, to treat a particular disease or condition, the siNA molecules can be administered to a subject or can be administered to other appropriate cells evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic agents to treat a disease or condition. Non-limiting examples of other therapeutic agents that can be readily combined with a siNA molecule of the invention are enzymatic nucleic acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and other organic and/or inorganic compounds including metals, salts and ions.

In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.,* 2002, *Nature Biotechnology,* 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology,* 19, 497; Lee *et al.,* 2002, *Nature*

Biotechnology, 19, 500; and Novina *et al.,* 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siRNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession number in Table III.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siRNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession number in Table III) are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group, remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

Figure 2 shows a MALDI-TOV mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

Figure 3 shows the results of a stability assay used to determine the serum stability of chemically modified siNA constructs compared to a siNA control consisting of all RNA with 3'-TT termini. T ½ values are shown for duplex stability.

Figure 4 shows the results of an RNAi activity screen of phosphorothioate modified siNA constructs using a luciferase reporter system.

Figure 5 shows the results of an RNAi activity screen of phosphorothioate and universal base modified siNA constructs using a luciferase reporter system.

Figure 6 shows the results of an RNAi activity screen of 2'-O-methyl modified siNA constructs using a luciferase reporter system.

Figure 7 shows the results of an RNAi activity screen of 2'-O-methyl and 2'-deoxy-2'-fluoro modified siNA constructs using a luciferase reporter system.

Figure 8 shows the results of an RNAi activity screen of a phosphorothioate modified siNA construct using a luciferase reporter system.

Figure 9 shows the results of an RNAi activity screen of an inverted deoxyabasic modified siNA construct generated via tandem synthesis using a luciferase reporter system.

Figure 10 shows the results of an RNAi activity screen of chemically modifed siNA constructs including 3'-glyceryl modified siNA constructs compared to an all RNA control siNA construct using a luciferase reporter system. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I.

Figure 11 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I.

Figure 12 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. In addition, the antisense strand alone (RPI 30430) and an inverted control (RPI 30227/30229, having matched chemistry to RPI 30063/30224) was compared to the siNA duplexes described above.

Figure 13 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. In addition, an inverted control (RPI 30226/30229, having matched chemistry to RPI 30222/30224) was compared to the siNA duplexes described above.

Figure 14 shows the results of an RNAi activity screen of chemically modifed siNA constructs including various 3'-terminal modified siNA constructs compared to an all RNA control siNA construct using a luciferase reporter system. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI

number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I.

Figure 15 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemistries compared to a fixed antisense strand chemistry. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I.

Figure 16 shows the results of a siNA titration study wherein the RNAi activity of a phosphorothioate modified siNA construct is compared to that of a siNA construct consisting of all ribonucleotides except for two terminal thymidine residues using a luciferase reporter system.

Figure 17 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directely into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

Figure 18A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be substituted in the overhanging regions designated by parenthesis (N N). Various modifications are shown for the sense and antisense strands of the siNA constructs.

Figure 18A: The sense strand comprises 21 nucleotides having four phosphorothioate 5'- and 3'-terminal internucleotide linkages, wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and four 5'-terminal phosphorothioate internucleotide linkages and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 18B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 18C: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-

deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 18D: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 18E: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein.

Figure 18F: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified

nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-deoxy modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand of constructs A-F comprise sequence complementary to target RNA sequence of the invention.

Figure 19 shows non-limiting examples of specific chemically modified siNA sequences of the invention. **A-F** applies the chemical modifications described in **Figure 18A-F** to a representative siNA sequence targeting the EGFR (HER1).

Figure 20 shows non-limiting examples of different siNA constructs of the invention. The examples shown (constructs 1, 2, and 3) have 19 representative base pairs, however, different embodiments of the invention include any number of base pairs described herein. Bracketed regions represent nucleotide overhangs, for example comprising between about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 in vivo and/or in vitro. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 in vivo and/or in vitro, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 in vivo and/or in vitro. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use in vivo or in vitro and/or in vitro.

Figure 21 is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as

messenger RNA. (A) A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA. (B) The sequences are transfected into cells. (C) Cells are selected based on phenotypic change that is associated with modulation of the target nucleic acid sequence. (D) The siNA is isolated from the selected cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

Figure 22 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including **(1)** [3-3']-inverted deoxyribose; **(2)** deoxyribonucleotide; **(3)** [5'-3']-3'-deoxyribonucleotide; **(4)** [5'-3']-ribonucleotide; **(5)** [5'-3']-3'-O-methyl ribonucleotide; **(6)** 3'-glyceryl; **(7)** [3'-5']-3'-deoxyribonucleotide; **(8)** [3'-3']-deoxyribonucleotide; **(9)** [5'-2']-deoxyribonucleotide; and **(10)** [5-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

Figure 23 shows a non-limiting example of siNA mediated inhibition of VEGF-induced angiogenesis using the rat corneal model of angiogenesis. siNA targeting site 2340 of VEGFR1 RNA (shown as RPI No. sense strand/antisense strand) were compared to inverted controls (shown as RPI No. sense strand/antisense strand) at three different concentrations and compared to a VEGF control in which no siNA was administered.

Figure 24 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-mofications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct in tested in an appropriate system (e.g human serum for nuclease

resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

Figure 25 shows a non-limiting example of reduction of HER2 mRNA in A549 cells mediated by RNA-based and chemically-modified siNAs that target HER2 mRNA sites 2344 and 3706. A549 cells were transfected with 4 ug/ml lipid complexed with 25 nM unmodified siNA with a 3'-terminal dithymidine cap (RPI#28266/28267) or a corresponding inverted control (RPI#28268/28269) for site 2344 and (RPI#28262/28263) and a corresponding inverted control (RPI 28264/28265) for site 3706. In addition, A549 cells were transfected with 4 ug/ml lipid complexed with 25 nM modified siNA (RPI#30442/30443) and a corresponding matched control (RPI#30444/30445) for site 2344 and (RPI#30438/30439) and a corresponding matched control (RPI 30440/30441) for site 3706. As shown in the figures, the modified and unmodified constructs targeting sites 2344 and 3706 all demonstrate significant inhibition of HER2 RNA expression.

Figure 26 shows a non-limiting example of reduction of PKC-alpha mRNA in A549 cells mediated by chemically-modified siNAs that target PKC-alpha mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, all of the siNA constructs show significant reduction of PKC-alpha RNA expression.

Figure 27 shows a non-limiting example of reduction of Myc (c-Myc) mRNA in 293T cells mediated by chemically-modified siNAs that target c-Myc mRNA. 293T cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, three

of the siNA constructs (RPI 30993/31069; RPI 30995/31071; and RPI 30996/31072) show significant reduction of c-Myc RNA expression.

Figure 28 shows a non-limiting example of reduction of BCL2 mRNA in A549 cells mediated by chemically-modified siNAs that target BCL2 mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#30998/31074) was tested along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31368/31369), which was also compared to a matched chemistry inverted control (RPI#31370/31371) and a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine and 2'-deoxy-2'-fluoro purine nucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31372/31373) which was also compared to a matched chemistry inverted control (RPI#31374/31375). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, the siNA constructs show significant reduction of BCL2 RNA expression compared to scrambled, untreated, and transfection controls.

Figure 29 shows a non-limiting example of reduction of CHK-1 mRNA in A549 cells mediated by chemically-modified siNAs that target CHK-1 mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31003/31079) and a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and in which the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31302/31303), were compared to a matched chemistry inverted control (RPI#31314/31325). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2),

and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs show significant reduction of CHK-1 RNA expression compared to appropriate controls.

Figure 30 shows a non-limiting example of reduction of BACE mRNA in A549 cells mediated by siNAs that target BACE mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, all of the siNA constructs show significant reduction of BACE RNA expression.

Figure 31 shows a non-limiting example of reduction of cyclin D1 mRNA in A549 cells mediated by chemically-modified siNAs that target cyclin D1 mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31009/31085) was compared to a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31304/31305), which was also compared to a matched chemistry inverted control (RPI#31316/31317). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs show significant reduction of cyclin D1 RNA expression.

Figure 32 shows a non-limiting example of reduction of PTP-1B mRNA in A549 cells mediated by chemically-modified siNAs that target PTP-1B mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31018/31307) was compared to a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage

(RPI#31306/31307), which was also compared to a matched chemistry inverted control (RPI#31318/31319). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs show significant reduction of PTP-1B RNA expression.

Figure 33 shows a non-limiting example of reduction of ERG2 mRNA in DLD1 cells mediated by siNAs that target ERG2 mRNA. DLD1 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A screen of siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, all of the siNA constructs show significant reduction of ERG2 RNA expression.

Figure 34 shows a non-limiting example of reduction of PCNA mRNA in A549 cells mediated by chemically-modified siNAs that target PCNA mRNA. A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31035/31111) was compared to a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31310/31311), which was also compared to a matched chemistry inverted control (RPI#31322/31323). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs show significant reduction of PCNA RNA expression.

DETAILED DESCRIPTION OF THE INVENTION

Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-

modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or "improved RNAi activity" is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature,* 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response though a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Berstein *et al.*, 2001, *Nature,* 409, 363). Short interfering RNAs derived from Dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has

also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.,* 2001, *Science,* 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.,* 2001, *Genes Dev.,* 15, 188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing, presumably though cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science,* 297, 1818-1819; Volpe *et al.,* 2002, *Science,* 297, 1833-1837; Jenuwein, 2002, *Science,* 297, 2215-2218; and Hall *et al.,* 2002, *Science,* 297, 2232-2237). As such, siNA molecules of the invention can be used to mediate gene silencing via interaction with RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.,* 1998, *Nature,* 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.,* 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.,* 2000, *Nature,* 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.,* 2001, *Nature,* 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in Drosophila embryonic lysates has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end

(Elbashir *et al.,* 2001, *EMBO J.,* 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.,* 2001, *Cell,* 107, 309); however, siRNA molecules lacking a 5'-phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs "small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.,* 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.,* International PCT Publication No. WO 99/54459, Wincott *et al.,* 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.,* 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.,* 1998, *Biotechnol Bioeng.,* 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. **Table II** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene

(Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μL of 0.11 M = 6.6 μmol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μL of 0.25 M = 15 μmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μL of 0.11 M = 4.4 μmol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μL of 0.25 M = 10 μmol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I_2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 7.5 min coupling step for alkylsilyl

protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. **Table II** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μL of 0.11 M = 6.6 μmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 μL of 0.25 M = 15 μmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 μL of 0.11 M = 13.2 μmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 μL of 0.25 M = 30 μmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I_2, 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 μL of a solution of 1.5 mL N-methylpyrrolidinone, 750 μL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH_4HCO_3.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 min. The vial is brought to rt. TEA•3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 min. The sample is cooled at –20 °C and then quenched with 1.5 M NH_4HCO_3.

For purification of the trityl-on oligomers, the quenched NH_4HCO_3 solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 min. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.,* 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore *et al.,* 1992, *Science* 256, 9923; Draper *et al.,* International PCT publication No. WO 93/23569; Shabarova *et al.,* 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.,* 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.,* 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as

described herein can also be readily adapted to large scale synthesis platforms employing batch reactors, synthesis columns and the like.

A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

The nucleic acid molecules of the present invention can be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-fluoro, 2'-*O*-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.,* 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott *et al., supra*, the totality of which is hereby incorporated herein by reference) and re-suspended in water.

In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) can prevent their degradation by serum ribonucleases, which can increase their potency (see *e.g.,* Eckstein *et al.,* International Publication No. WO 92/07065; Perrault *et al.,* 1990 *Nature* 344, 565; Pieken *et al.,* 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.,* International Publication No. WO 93/15187; and Rossi *et al.,* International Publication No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.,* U.S. Pat. No. 6,300,074; and Burgin *et al., supra;* all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein.

Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-fluoro, 2'-*O*-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS.* 17, 34; Usman *et al.,* 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.,* 1996, *Biochemistry,* 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein *et al., International Publication* PCT No. WO 92/07065; Perrault *et al. Nature,* 1990, *344,* 565-568; Pieken *et al. Science,* 1991, *253,* 314-317; Usman and Cedergren, *Trends in Biochem. Sci.* , 1992, *17,* 334-339; Usman *et al. International Publication* PCT No. WO 93/15187; Sproat, *U.S. Pat.* No. 5,334,711 and Beigelman *et al.,* 1995, *J. Biol. Chem.,* 270, 25702; Beigelman *et al.,* International PCT publication No. WO 97/26270; Beigelman *et al.,* U.S. Pat. No. 5,716,824; Usman *et al.,* U.S. Pat. No. 5,627,053; Woolf *et al.,* International PCT Publication No. WO 98/13526; Thompson *et al.,* USSN 60/082,404 which was filed on April 20, 1998; Karpeisky *et al.,* 1998, *Tetrahedron Lett.,* 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences),* 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.,* 67, 99-134; and Burlina *et al.,* 1997, *Bioorg. Med. Chem.,* 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi is cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity.

Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.,* 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.,* 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

In one embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.,* 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.,* International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

The term "biodegradable linker" as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single

nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

Therapeutic nucleic acid molecules (*e.g.,* siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

Use of the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple siNA molecules targeted to different genes; nucleic acid molecules coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'- cap structure, for example on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety.

In non-limiting examples, the 3'-cap is selected from the group consisting of glyceryl, inverted deoxy abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2, halogen, $N(CH_3)_2$, amino, or SH. The term "alkyl" also includes alkynyl groups that have an

unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO_2 or $N(CH_3)_2$, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.,* International PCT Publication No. WO 92/07065; Usman *et al.,* International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra,* all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.,* 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-

limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.,* 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties,* in *Modern Synthetic Methods,* VCH, 331-417, and Mesmaeker *et al.,* 1994, *Novel Backbone Replacements for Oligonucleotides,* in *Carbohydrate Modifications in Antisense Research,* ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.,* U.S. Pat. No. 5,998,203.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β-D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH_2 or 2'-*O*- NH_2, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.,* U.S. Pat. No. 5,672,695

and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro,* stability, and ease of introduction of such oligonucleotides to the target site, *e.g.,* to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Nucleic Acid Molecules

A siNA molecule of the invention can be adapted for use to treat any disease, infection or condition associated with gene expression, and other indications that can respond to the level of gene product in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.,* 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer *et al.,* 1999, *Mol. Membr. Biol.,* 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.,* 137, 165-192; and Lee *et al.,* 2000, *ACS Symp. Ser.,* 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.,* U.S. Pat. No. 6,395,713 and Sullivan *et al.,* PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins (see for example Gonzalez *et al.,* 1999, *Bioconjugate Chem.,* 10, 1068-1074), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can take place using standard needle and syringe methodologies, or by needle-free technologies

such as those described in Conry *et al.,* 1999, *Clin. Cancer Res.,* 5, 2330-2337 and Barry *et al.,* International PCT Publication No. WO 99/31262. Many examples in the art describe CNS delivery methods of oligonucleotides by osmotic pump, (see Chun *et al.,* 1998, *Neuroscience Letters,* 257, 135-138, D'Aldin *et al.,* 1998, *Mol. Brain Research,* 55, 151-164, Dryden *et al.,* 1998, *J. Endocrinol.,* 157, 169-175, Ghirnikar *et al.,* 1998, *Neuroscience Letters,* 247, 21-24) or direct infusion (Broaddus *et al.,* 1997, *Neurosurg. Focus,* 3, article 4). Other routes of delivery include, but are not limited to oral (tablet or pill form) and/or intrathecal delivery (Gold, 1997, *Neuroscience,* 76, 1153-1158). More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan *et al.*, supra, Draper *et al.*, PCT WO93/23569, Beigelman *et al.,* PCT WO99/05094, and Klimuk *et al.,* PCT WO99/04819 all of which have been incorporated by reference herein. The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

In addition, the invention features the use of methods to deliver the nucleic acid molecules of the instant invention to hematopoietic cells, including monocytes and lymphocytes. These methods are described in detail by Hartmann *et al.,* 1998, *J. Phamacol. Exp. Ther.,* 285(2), 920-928; Kronenwett *et al.,* 1998, *Blood,* 91(3), 852-862; Filion and Phillips, 1997, *Biochim. Biophys. Acta.,* 1329(2), 345-356; Ma and Wei, 1996, *Leuk. Res.,* 20(11/12), 925-930; and Bongartz *et al.,* 1994, *Nucleic Acids Research,* 22(22), 4681-8. Such methods, as described above, include the use of free oligonucleitide, cationic lipid formulations, liposome formulations including pH sensitive liposomes and immunoliposomes, and bioconjugates including oligonucleotides conjugated to fusogenic peptides, for the transfection of hematopoietic cells with oligonucleotides.

Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as

tablets, capsules or elixirs for oral administration, suppositories for rectal administration, sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or subject, including for example a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to which the negatively charged nucleic acid is desirable for delivery). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess MDR.

By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Jolliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF *et al*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al.*,1995, *Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 42, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*,

International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (*e.g.*, intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical

compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monosterate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as

polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable

dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and

drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly depends on the degree of branching of the oligosaccharide chain, for example, triatennary structures are bound with greater affinity than biatenarry or monoatennary chains (Baenziger and Fiete, 1980, *Cell,* 22, 611-620; Connolly *et al.,* 1982, *J. Biol. Chem.,* 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.,* 1981, *J. Med. Chem.,* 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavialability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese *et al.,* USSN 10/201,394, filed August 13, 2001; and Matulic-Adamic *et al.,* USSN 60/362,016, filed March 6, 2002.

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (*e.g.*, Izant and Weintraub, 1985, *Science,* 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J. Virol.*, 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science,* 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol. Chem.*, 269, 25856.

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.,* 2002, *Nature Biotechnology,* 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology,* 19, 497; Lee *et al.,* 2002, *Nature Biotechnology,* 19, 500; and Novina *et al.,* 2002, *Nature Medicine,* advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (*e.g.,* eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.,* eukaryotic pol I, II or III termination region); and c) a nucleic acid sequence encoding at least one of the siNA molecules of the instant invention; wherein said sequence is operably linked to said initiation region and said termination region, in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the invention; and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. U S A,* 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber *et al.,* 1993, *Methods Enzymol.,* 217, 47-66; Zhou *et al.,* 1990, *Mol. Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet *et al.,* 1992, *Antisense Res. Dev.,* 2, 3-15; Ojwang *et al.,* 1992, *Proc. Natl. Acad. Sci. U S A,* 89, 10802-6; Chen *et al.,* 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.,* 1993, *Proc. Natl. Acad. Sci. U S A,* 90, 6340-4; L'Huillier *et al.,* 1992, *EMBO J.,* 11,

4411-8; Lisziewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A*, 90, 8000-4; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science,* 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson *et al., supra*; Couture and Stinchcomb, *1996, supra*; Noonberg *et al.,* 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.,* U.S. Pat. No. 5,624,803; Good *et al.,* 1997, *Gene Ther.,* 4, 45; Beigelman *et al.,* International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, *1996, supra).*

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the termination region in a manner that allows expression and/or delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

Examples:

The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

Example 1: Tandem synthesis of siNA constructs

Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example, a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example, by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexaflurorophosphate (PyBrOP). After the linker is coupled, standard synthesis chemistry is utilized to complete synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M $NH_4H_2CO_3$.

Purification of the siNA duplex can be readily accomplished using solid phase extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1 column volume (CV) of acetonitrile, 2 CV H2O, and 2 CV 50mM NaOAc. The sample is loaded and then washed with 1 CV H2O or 50mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The column is then washed, for example with 1 CV H2O followed by on-column detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with H20 followed by 1 CV 1M NaCl and additional H2O. The siNA duplex product is then eluted, for example, using 1 CV 20% aqueous CAN.

Figure 2 provides an example of MALDI-TOV mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA contract only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

Example 2: Serum stability of chemically modified siNA constructs

Chemical modifications were introduced into siNA constructs to determine the stability of these constructs compared to native siNA oligonucleotides (containing two thymidine nucleotide overhangs) in human serum. An investigation of the serum stability of RNA duplexes revealed that siNA constructs consisting of all RNA nucleotides containing two thymidine nucleotide overhangs have a half-life in serum of 15 seconds, whereas chemically modified siNA constructs remained stable in serum for 1 to 3 days depending on the extent of modification. RNAi stability tests were performed by internally labeling one strand (strand 1) of siNA and duplexing with 1.5 X the concentration of the complementary siNA strand (strand 2) (to insure all labeled material was in duplex form). Duplexed siNA constructs were then tested for stability by incubating at a final concentration of 2μM siNA (strand 2 concentration) in 90% mouse or human serum for time-points of 30sec, 1min, 5min, 30min, 90min, 4hrs 10min, 16hrs 24min, and 49hrs. Time points were run on a 15% denaturing polyacrylamide gels and analyzed on a phosphoimager.

Internal labeling was performed via kinase reactions with polynucleotide kinase (PNK) and ^{32}P-γ-ATP, with addition of radiolabeled phosphate at nucleotide 13 of strand 2, counting in from the 3' side. Ligation of the remaining 8-mer fragments with T4 RNA ligase resulted in the full length, 21-mer, strand 2. Duplexing of RNAi was done by adding appropriate concentrations of the siNA oligonucleotides and heating to 95° C for 5min followed by slow cooling to room temperature. Reactions were performed by adding 100% serum to the siNA duplexes and incubating at 37° C, then removing aliquots at desired time-points. Results of this study are summarized in **Figure 3**. As shown in the Figure 3, chemically modified siNA molecules (e.g., SEQ ID NOs: 925/927, 925/928, 925/929, 925/930, and 925/931) have significantly increased serum stability compared to an siNA construct having all ribonucleotides except a 3'-terminal dithymidine (TT) modification (e.g., SEQ ID NOs: 925/926).

Example 3: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to

the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays or combinatorial/siNA library screening assays to determine efficient reduction in target gene expression.

Example 4: Selection of siNA molecule target sites in a RNA

The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

The target sequence is parsed in silico into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.

In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each

list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.

In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.

The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.

The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.

The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever other appropriately suitable sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.

The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.

Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper (sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see Tables I). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.

The siNA molecules are screened in an in vitro, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

In an alternate approach, a pool of siNA constructs specific to a target sequence is used to screen for target sites in cells expressing target RNA, such as human HeLa cells. The general strategy used in this approach is shown in **Figure 21**. A non-limiting example of such as pool is a pool comprising sequences having antisense sequences complementary to the target RNA sequence and sense sequences complementary to the antisense sequences. Cells (e.g., HeLa cells) expressing the target gene are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with gene silencing are sorted. The pool of siNA constructs can be chemically modified as described herein and synthesized, for example, in a high throughput manner. The siNA from cells demonstrating a positive phenotypic change (e.g., decreased target mRNA levels or target protein expression), are identified, for example by positional analysis within the assay, and are used to determine the most suitable target site(s) within the target RNA sequence based upon the complementary sequence to the corresponding siNA antisense strand identified in the assay.

Example 5: RNAi activity of chemically modified siNA constructs

Short interfering nucleic acid (siNA) is emerging as a powerful tool for gene regulation. All-ribose siNA duplexes activate the RNAi pathway but have limited utility as therapeutic compounds due to their nuclease sensitivity and short half-life in serum, as shown in Example 2 above. To develop nuclease-resistant siNA constructs for *in vivo*

applications, siNAs that target luciferase mRNA and contain stabilizing chemical modifications were tested for activity in HeLa cells. The sequences for the siNA oligonucleotide sequences used in this study are shown in **Table I**. Modifications included phosphorothioate linkages (P=S), 2'–*O*–methyl nucleotides, or 2'–fluoro (F) nucleotides in one or both siNA strands and various 3'-end stabilization chemistries, including 3'-glyceryl, 3'-inverted abasic, 3'-inverted Thymidine, and/or Thymidine. Active siNA containing stabilizing modifications such as described herein should prove useful for *in vivo* applications.

A luciferase reporter system was utilized to test RNAi activity of chemically modified siNA constructs compared to siNA constructs consisting of all RNA nucleotides containing two thymidine nucleotide overhangs. Sense and antisense siNA strands (20 uM each) were annealed by incubation in buffer (100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 min. at 90°C followed by 1 hour at 37°C. Plasmids encoding firefly luciferase (pGL2) and renilla luciferase (pRLSV40) were purchased from Promega Biotech.

HeLa S3 cells were grown at 37°C in DMEM with 5% FBS and seeded at 15,300 cells in 100 ul media per well of a 96-well plate 24 hours prior to transfection. For transfection, 4 ul Lipofectamine 2000 (Life Technologies) was added to 96 ul OPTI-MEM, vortexed and incubated at room temperature for 5 minutes. The 100 ul diluted lipid was then added to a microtiter tube containing 5 ul pGL2 (200ng/ul), 5 ul pRLSV40 (8 ng/ul) 6 ul siNA (25 nM or 10 nM final), and 84 ul OPTI-MEM, vortexed briefly and incubated at room temperature for 20 minutes. The transfection mix was then mixed briefly and 50 ul was added to each of three wells that contained HeLa S3 cells in 100 ul media. Cells were incubated for 20 hours after transfection and analyzed for luciferase expression using the Dual luciferase assay according to the manufacturer's instructions (Promega Biotech). The results of this study are summarized in **Figures 4-16**. The sequences of the siNA strands used in this study are shown in Table I and are referred to by RPI# in the figures. Normalized luciferase activity is reported as the ratio of firefly luciferase activity to renilla luciferase activity in the same sample. Error bars represent standard deviation of triplicate transfections. As shown in **Figures 4-16**, the RNAi activity of chemically modified constructs is comparable to that of control siNA constructs, which consist of all ribonucleotides at every position except the 3'-terminus

which comprises two thymidine nucleotide overhangs. In some instances, the RNAi activity of the chemically modified constructs is greater than the siNA construct consisting of all ribonucleotides at every position except the 3'-terminus which comprises two thymidine nucleotide overhangs. For example, **Figure 4** shows results obtained from a screen using phosphorothioate modified siNA constructs; the RPI 27654/27659 construct contains phosphorothioate substitutions for every pyrimidine nucleotide in both sequences, the RPI 27657/27662 construct contains 5 terminal 3'-phosphorothioate substitutions in each strand, the RPI 27649/27658 construct contains all phosphorothioate substitutions only in the antisense strand, whereas the RPI 27649/27660 and RPI 27649/27661 constructs have unmodified sense strands and varying degrees of phosphorothioate substitutions in the antisense strand. All of these constructs show significant RNAi activity when compared to a scrambled siNA.

Figure 5 shows results obtained from a screen using phosphorothioate (RPI 28253/28255 and RPI 28254/28256) and universal base substitutions (RPI 28257/28259 and RPI 28258/28260) compared to the same controls described above. As shown, these modifications show equivalent or better RNAi activity when compared to the control siNA construct.

Figure 6 shows results obtained from a screen using 2'-O-methyl modified siNA constructs in which the sense strand contains either 10 (RPI 28244/27650) or 5 (RPI 28245/27650) 2'-O-methyl substitutions, both with comparable activity to the control siNA construct.

Figure 7 shows results obtained from a screen using 2'-O-methyl or 2'-deoxy-2'-fluoro modified siNA constructs compared to a control construct consisting of all ribonucleotides at every position except the 3'-terminus which comprises two thymidine nucleotide overhangs.

Figure 8 compares a siNA construct containing six phosphorothioate substitutions in each strand (RPI 28460/28461), where 5 phosphorothioates are present at the 3' end and a single phosphorothioate is present at the 5' end of each strand. This motif shows very similar activity to the control siNA construct consisting of all ribonucleotides at every position except the 3'-terminus which comprises two thymidine nucleotide overhangs.

Figure 9 compares a siNA construct synthesized by the method of the invention described in Example 1, wherein an inverted deoxyabasic succinate linker was used to generate a siNA having a 3'-inverted deoxyabasic cap on the antisense strand of the siNA. This construct shows improved activity compared to the control siNA (siGL2) construct consisting of all ribonucleotides at every position except the 3'-terminus which comprises two thymidine nucleotide overhangs.

Figure 10 shows the results of an RNAi activity screen of chemically modifed siNA constructs including 3'-glyceryl modified siNA constructs compared to an all RNA control siNA construct using a luciferase reporter system. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. As shown in the Figure, the 3'-terminal modified siNA constructs retain significant RNAi activity compared to the control siNA (siGL2) construct.

Figure 11 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. As shown in the figure, the chemically modified RPI 30063/30430, RPI 30433/30430, and RPI 30063/30224 constructs retain significant RNAi activity compared to the control siNA construct. It should be noted that RPI 30433/30430 is a siNA construct having no ribonucleotides which retains significant RNAi activity compared to the constrol siGL2 construct in vitro, therefore, this construct is expected to

have both similar RNAi activity and improved stability compared to siNA constructs having ribonucleotides in vivo.

Figure 12 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. As shown in the figure, the chemically modified RPI 30063/30224 and RPI 30063/30430 constructs retain significant RNAi activity compared to the control siNA (siGL2) construct. In addition, the antisense strand alone (RPI 30430) and an inverted control (RPI 30227/30229, having matched chemistry to RPI 30063/30224) were compared to the siNA duplexes described above. The antisense strand (RPI 30430) alone provides far less inhibition compared to the siNA duplexes using this sequence.

Figure 13 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemical modifications and antisense strand chemical modifications. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. In addition, an inverted control (RPI 30226/30229, having matched chemistry to RPI 30222/30224) was compared to the siNA duplexes described above. As shown in the figure, the chemically modified RPI 28251/30430, RPI 28251/30224, and RPI 30222/30224 constructs retain significant RNAi activity compared to the control siNA construct, and the chemically modified RPI 28251/30430 construct demonstrates improved activity compared to the control siNA (siGL2) construct.

Figure 14 shows the results of an RNAi activity screen of chemically modifed siNA constructs including various 3'-terminal modified siNA constructs compared to an all RNA control siNA construct using a luciferase reporter system. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. As shown in the figure, the chemically modified RPI 30222/30546, 30222/30224, 30222/30551, 30222/30557 and 30222/30558 constructs retain significant RNAi activity compared to the control siNA construct.

Figure 15 shows the results of an RNAi activity screen of chemically modifed siNA constructs. The screen compared various combinations of sense strand chemistries compared to a fixed antisense strand chemistry. These chemically modified siNAs were compared in the luciferase assay described herein at 1 nM and 10nM concentration using an all RNA siNA control (siGL2) having having 3'-terminal dithymidine (TT) and its corresponding inverted control (Inv siGL2). The background level of luciferase expression in the HeLa cells is designated by the "cells" column. Sense and antisense strands of chemically modified siNA constructs are shown by RPI number (sense strand/antisense strand). Sequences correspoding to these RPI numbers are shown in Table I. As shown in the figure, the chemically modified RPI 30063/30430, 30434/30430, and 30435/30430 constructs all demonstrate greater activity compared to the control siNA (siGL2) construct.

Example 6: RNAi activity titration

A titration assay was performed to determine the lower range of siNA concentration required for RNAi activity both in a control siNA construct consisting of all RNA nucleotides containing two thymidine nucleotide overhangs and a chemically modified siNA construct comprising 5 phosphorothioate internucleotide linkages in both the sense and antisense strands. The assay was performed as described above, however, the siNA constructs were diluted to final concentrations between 2.5 nM and 0.025 nM. Results

are shown in **Figure 16**. As shown in **Figure 16**, the chemically modified siNA construct shows a very similar concentration dependent RNAi activity profile to the control siNA construct when compared to an inverted siNA sequence control.

Example 7: siNA design

siNA target sites were chosen by analyzing sequences of the target RNA and optionally prioritizing the target sites on the basis of folding (structure of any given sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 4, or alternately by using an *in vitro* siNA system as described in Example 9 herein. siNA molecules were designed that could bind each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantity RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 24**).

Example 8: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can by synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.,* US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.,* US Patent Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoroamidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine, N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2′-O-Silyl Ethers can be used in conjunction with acid-labile 2′-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.,* US Patent 5,631,360, incorporated by reference herein in its entirety).

During solid phase synthesis, each nucleotide is added sequentially (3′- to 5′-direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3′-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5′-end of the first nucleoside. The support is then washed and any unreacted 5′-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5′-acetyl moieties. The trivalent phosphorus linkage is

then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition cycle, the 5′-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency, for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Usman et al., US 5,831,071, US 6,353,098, US 6,437,117, and Bellon et al., US 6,054,576, US 6,162,909, US 6,303,773, incorporated by reference herein in their entirety or Scaringe *supra*,. Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides can degrade under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

Example 9: RNAi *in vitro* assay to assess siNA activity

An in vitro assay that recapitulates RNAi in a cell free system is used to evaluate siNA constructs specific to target RNA. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with target RNA. A Drosophila extract derived from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*. Target RNA is generated via *in vitro* transcription from an appropriate plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 min. at 90°C followed by 1 hour at 37°C , then diluted in lysis buffer (for example 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate). Annealing

can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The Drosophila lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug.ml creatine phosphokinase, 100 um GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25 x Passive Lysis Buffer (Promega). Target RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in which siNA is omitted from the reaction.

Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [alpha-^{32}P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'-^{32}P-end labeled using T4 polynucleotide kinase enzyme. Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager® quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

In one embodiment, this assay is used to determine target sites the RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the RNA target, for example, by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

Example 10: Nucleic acid inhibition of target RNA *in vivo*

siNA molecules targeted to the target RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity *in vivo*, for example, using the following procedure.

Two formats are used to test the efficacy of siNAs targeting a particular gene transcipt. First, the reagents are tested on target expressing cells (e.g., HeLa), to determine the extent of RNA and protein inhibition. siNA reagents are selected against the RNA target. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (*eg.*, ABI 7700 Taqman®). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

Delivery of siNA to Cells

Cells (e.g., HeLa) are seeded, for example, at $1x10^5$ cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20nM) and cationic lipid (e.g., final concentration 2μg/ml) are complexed in EGM basal media (Biowhittaker) at 37°C for 30 mins in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at $1x10^3$ in 96 well plates and siNA complex added as described. Efficiency of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

Taqman and Lightcycler quantification of mRNA

Total RNA is prepared from cells following siNA delivery, for example, using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For

Taqman analysis, dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence Detector using 50 µl reactions consisting of 10 µl total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM $MgCl_2$, 300 µM each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AmpliTaq Gold (PE-Applied Biosystems) and 10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 min at 48°C, 10 min at 95°C, followed by 40 cycles of 15 sec at 95°C and 1 min at 60°C. Quantitation of mRNA levels is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/rxn) and normalizing to ß-actin or GAPDH mRNA in parallel TaqMan reactions. For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of SYBR Green I dye into a specific PCR product can be measured in glass capillary tubes using a lightcyler. A standard curve is generated for each primer pair using control cRNA. Values are represented as relative expression to GAPDH in each sample.

Western blotting

Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research,* 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

Example 11: Animal Models

Various animal models can be used to screen siNA constructs *in vivo* as are known in the art, for example those animal models that are used to evaluate other nucleic acid technologies such as enzymatic nucleic acid molecules (ribozymes) and/or antisense. Such animal models are used to test the efficacy of siNA molecules described herein. In a non-limiting example, siNA molecules that are designed as anti-angiogenic agents can be screened animal models. There are several animal models in which the anti-angiogenesis effect of nucleic acids of the present invention, such as siNA, directed against genes associated with angiogenesis and/or metastais, such as VEGFR (e.g., VEGFR1, VEGFR2, and VEGFR3) genes. Typically a corneal model has been used to study angiogenesis in rat and rabbit since recruitment of vessels can easily be followed in this normally avascular tissue (Pandey *et al.,* 1995 *Science* 268: 567-569). In these models, a small Teflon or Hydron disk pretreated with an angiogenesis factor (e.g. bFGF or VEGF) is inserted into a pocket surgically created in the cornea. Angiogenesis is monitored 3 to 5 days later. siNA molecules directed against VEGFR mRNAs are delivered in the disk as well, or dropwise to the eye over the time course of the experiment. In another eye model, hypoxia has been shown to cause both increased expression of VEGF and neovascularization in the retina (Pierce *et al.,* 1995 *Proc. Natl. Acad. Sci.* USA. 92: 905-909; Shweiki *et al.,* 1992 *J. Clin. Invest.* 91: 2235-2243).

Several animal models exist for screening of anti-angiogenic agents. These include corneal vessel formation following corneal injury (Burger *et al.,* 1985 *Cornea* 4: 35-41; Lepri, *et al.,* 1994 *J. Ocular Pharmacol.* 10: 273-280; Ormerod *et al.,* 1990 *Am. J. Pathol.* 137: 1243-1252) or intracorneal growth factor implant (Grant *et al.,* 1993 *Diabetologia* 36: 282-291; Pandey *et al.* 1995 *supra;* Zieche *et al.,* 1992 *Lab. Invest.* 67: 711-715), vessel growth into Matrigel matrix containing growth factors (Passaniti *et al.,* 1992 *supra*), female reproductive organ neovascularization following hormonal manipulation (Shweiki *et al.,* 1993 *Clin. Invest.* 91: 2235-2243), several models involving inhibition of tumor growth in highly vascularized solid tumors (O'Reilly *et al.,* 1994 *Cell* 79: 315-328; Senger *et al.,* 1993 *Cancer and Metas. Rev.* 12: 303-324; Takahasi *et al.,* 1994 *Cancer Res.* 54: 4233-4237; Kim *et al.,* 1993 *supra*), and transient hypoxia-induced neovascularization in the mouse retina (Pierce *et al.,* 1995 *Proc. Natl. Acad. Sci.* USA. 92: 905-909).gene

The cornea model, described in Pandey et al. *supra*, is the most common and well characterized anti-angiogenic agent efficacy screening model. This model involves an avascular tissue into which vessels are recruited by a stimulating agent (growth factor, thermal or alkalai burn, endotoxin). The corneal model would utilize the intrastromal corneal implantation of a Teflon pellet soaked in a VEGF-Hydron solution to recruit blood vessels toward the pellet which can be quantitated using standard microscopic and image analysis techniques. To evaluate their anti-angiogenic efficacy, ribozymes are applied topically to the eye or bound within Hydron on the Teflon pellet itself. This avascular cornea as well as the Matrigel model provide for low background assays. While the corneal model has been performed extensively in the rabbit, studies in the rat have also been conducted.

The mouse model (Passaniti et al., *supra*) is a non-tissue model which utilizes Matrigel, an extract of basement membrane (Kleinman et al., 1986) or Millipore® filter disk, which can be impregnated with growth factors and anti-angiogenic agents in a liquid form prior to injection. Upon subcutaneous administration at body temperature, the Matrigel or Millipore® filter disk forms a solid implant. VEGF embedded in the Matrigel or Millipore® filter disk is used to recruit vessels within the matrix of the Matrigel or Millipore® filter disk which can be processed histologically for endothelial cell specific vWF (factor VIII antigen) immunohistochemistry, Trichrome-Masson stain, or hemoglobin content. Like the cornea, the Matrigel or Millipore® filter disk are avascular; however, it is not tissue. In the Matrigel or Millipore® filter disk model, siNA molecules are administered within the matrix of the Matrigel or Millipore® filter disk to test their anti-angiogenic efficacy. Thus, delivery issues in this model, as with delivery of siNA molecules by Hydron- coated Teflon pellets in the rat cornea model, may be less problematic due to the homogeneous presence of the siNA within the respective matrix.

The Lewis lung carcinoma and B-16 murine melanoma models are well accepted models of primary and metastatic cancer and are used for initial screening of anti-cancer agents. These murine models are not dependent upon the use of immunodeficient mice, are relatively inexpensive, and minimize housing concerns. Both the Lewis lung and B-16 melanoma models involve subcutaneous implantation of approximately 10^6 tumor cells from metastatically aggressive tumor cell lines (Lewis lung lines 3LL or D122, LLc-

LN7; B-16-BL6 melanoma) in C57BL/6J mice. Alternatively, the Lewis lung model can be produced by the surgical implantation of tumor spheres (approximately 0.8 mm in diameter). Metastasis also may be modeled by injecting the tumor cells directly *i.v.*. In the Lewis lung model, microscopic metastases can be observed approximately 14 days following implantation with quantifiable macroscopic metastatic tumors developing within 21-25 days. The B-16 melanoma exhibits a similar time course with tumor neovascularization beginning 4 days following implantation. Since both primary and metastatic tumors exist in these models after 21-25 days in the same animal, multiple measurements can be taken as indices of efficacy. Primary tumor volume and growth latency as well as the number of micro- and macroscopic metastatic lung foci or number of animals exhibiting metastases can be quantitated. The percent increase in lifespan can also be measured. Thus, these models provide suitable primary efficacy assays for screening systemically administered siNA molecules and siNA formulations.

In the Lewis lung and B-16 melanoma models, systemic pharmacotherapy with a wide variety of agents usually begins 1-7 days following tumor implantation/inoculation with either continuous or multiple administration regimens. Concurrent pharmacokinetic studies can be performed to determine whether sufficient tissue levels of siNA can be achieved for pharmacodynamic effect to be expected. Furthermore, primary tumors and secondary lung metastases can be removed and subjected to a variety of *in vitro* studies (*i.e.* target RNA reduction).

In utilizing these models to assess siNA activity, VEGFR1, VEGFR2, and/or VEGFR3 protein levels can be measured clinically or experimentally by FACS analysis. VEGFR1, VEGFR2, and/or VEGFR3 encoded mRNA levels will be assessed by Northern analysis, RNase-protection, primer extension analysis and/or quantitative RT-PCR. siNA molecules that block VEGFR1, VEGFR2, and/or VEGFR3 protein encoding mRNAs and therefore result in decreased levels of VEGFR1, VEGFR2, and/or VEGFR3 activity by more than 20% *in vitro* can be thus identified.

Example 12: siNA-mediated inhibition of angiogenesis *in vivo*

The purpose of this study was to assess the anti-angiogenic activity of siNA targeted against VEGFR1 in the rat cornea model of VEGF induced angiogenesis (see above). These siNA molecules have matched inverted controls which are inactive since

they are not able to interact with the RNA target. The siNA molecules and VEGF were co-delivered using the filter disk method: Nitrocellulose filter disks (Millipore®) of 0.057 diameter were immersed in appropriate solutions and were surgically implanted in rat cornea as described by Pandey *et al., supra.*

The stimulus for angiogenesis in this study was the treatment of the filter disk with 30 μM VEGF which is implanted within the cornea's stroma. This dose yields reproducible neovascularization stemming from the pericorneal vascular plexus growing toward the disk in a dose-response study 5 days following implant. Filter disks treated only with the vehicle for VEGF show no angiogenic response. The siNA were co-adminstered with VEGF on a disk in two different siNA concentrations. One concern with the simultaneous administration is that the siNA would not be able to inhibit angiogenesis since VEGF receptors can be stimulated. However, Applicant has observed that in low VEGF doses, the neovascular response reverts to normal, suggesting that the VEGF stimulus is essential for maintaining the angiogenic response. Blocking the production of VEGF receptors using simultaneous administration of anti-VEGF-R mRNA siNA could attenuate the normal neovascularization induced by the filter disk treated with VEGF.

Materials and Methods:

Test Compounds and Controls

R&D Systems VEGF, carrier free at 75 μM in 82 mM Tris-Cl, pH 6.9

siNA, 1.67 μG/μL, SITE 2340 (SEQ ID NO: 2; SEQ ID NO: 6) sense/antisense

siNA, 1.67 μG/μL, INVERTED CONTROL FOR SITE 2340 (SEQ ID NO: 19; SEQ ID NO: 20) sense/antisense

siNA 1.67 μg/μL, Site 2340 (SEQ ID NO: 419; SEQ ID NO: 420) sense/antisense

Animals

Harlan Sprague-Dawley Rats, Approximately 225-250g

45 males, 5 animals per group.

Husbandry

Animals are housed in groups of two. Feed, water, temperature and humidity are determined according to Pharmacology Testing Facility performance standards (SOP's) which are in accordance with the 1996 Guide for the Care and Use of Laboratory Animals (NRC). Animals are acclimated to the facility for at least 7 days prior to experimentation. During this time, animals are observed for overall health and sentinels will be bled for baseline serology.

Experimental Groups

Each solution (VEGF and siNAs) was prepared as a **1X** solution for final concentrations shown in the experimental groups described in **Table III**.

siNA Annealing Conditions

siNA sense and antisense strands are annealed for 1 minute in H_2O at 1.67mg/mL/strand followed by a 1 hour incubation at 37°C producing 3.34 mg/mL of duplexed siNA. For the 20µg/eye treatment, 6 µLs of the 3.34 mg/mL duplex is injected into the eye (see below). The 3.34 mg/mL duplex siNA can then be serially diluted for dose response assays.

Preparation of VEGF Filter Disk

For corneal implantation, 0.57 mm diameter nitrocellulose disks, prepared from 0.45 µm pore diameter nitrocellulose filter membranes (Millipore Corporation), were soaked for 30 min in 1 µL of 75 µM VEGF in 82 mM Tris·HCl (pH 6.9) in covered petri dishes on ice. Filter disks soaked only with the vehicle for VEGF (83 mM Tris-Cl pH 6.9) elicit no angiogenic response.

Corneal surgery

The rat corneal model used in this study was a modified from Koch *et al. Supra* and Pandey *et al., supra*. Briefly, corneas were irrigated with 0.5% povidone iodine solution followed by normal saline and two drops of 2% lidocaine. Under a dissecting microscope (Leica MZ-6), a stromal pocket was created and a presoaked filter disk (see above) was inserted into the pocket such that its edge was 1 mm from the corneal limbus.

Intraconjunctival injection of test solutions

Immediately after disk insertion, the tip of a 40-50 μm OD injector (constructed in our laboratory) was inserted within the conjunctival tissue 1 mm away from the edge of the corneal limbus that was directly adjacent to the VEGF-soaked filter disk. Six hundred nanoliters of test solution (siNA, inverted control or sterile water vehicle) were dispensed at a rate of 1.2 μL/min using a syringe pump (Kd Scientific). The injector was then removed, serially rinsed in 70% ethanol and sterile water and immersed in sterile water between each injection. Once the test solution was injected, closure of the eyelid was maintained using microaneurism clips until the animal began to recover gross motor activity. Following treatment, animals were warmed on a heating pad at 37°C.

Quantitation of angiogenic response

Five days after disk implantation, animals were euthanized following im administration of 0.4 mg/kg atropine and corneas were digitally imaged. The neovascular surface area (NSA, expressed in pixels) was measured *postmortem* from blood-filled corneal vessels using computerized morphometry (Image Pro Plus, Media Cybernetics, v2.0). The individual mean NSA was determined in triplicate from three regions of identical size in the area of maximal neovascularization between the filter disk and the limbus. The number of pixels corresponding to the blood-filled corneal vessels in these regions was summated to produce an index of NSA. A group mean NSA was then calculated. Data from each treatment group were normalized to VEGF/siNA vehicle-treated control NSA and finally expressed as percent inhibition of VEGF-induced angiogenesis.

Statistics

After determining the normality of treatment group means, group mean percent inhibition of VEGF-induced angiogenesis was subjected to a one-way analysis of variance. This was followed by two post-hoc tests for significance including Dunnett's (comparison to VEGF control) and Tukey-Kramer (all other group mean comparisons) at alpha = 0.05. Statistical analyses were performed using JMP v.3.1.6 (SAS Institute).

Results are graphically represented in **Figure 23**. As shown in **Figure 23**, VEGFR1 site 4229 active siNA at three concentrations were effective at inhibiting angiogenesis compared to the inverted siNA control and the VEGF control. A chemically modified version of the VEGFR1 site 4229 active siNA comprising a sense strand having 2'-deoxy-2'-fluoro pyrimidines and ribo purines with 5' and 3' terminal inverted deoxyabasic residues (SEQ ID NO: 419) and an antisense strand having having 2'-deoxy-2'-fluoro pyrimidines and ribo purines with a terminal 3'-phosphorothioate internucleotide linkage (SEQ ID NO: 420), showed similar inhibition. This result shows siNA molecules of differing chemically modified composition of the invention are capable of significantly inhibiting angiogenesis *in vivo*.

Example 13: RNAi mediated inhibition of EGFR (HER1) RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing EGFR (HER1) RNA expression in A549 cells. A549 cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37°C for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells wre lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and the percent reduction

of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 25.** A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#30988/31064) was compared to a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31300/31301), which was also compared to a matched chemistry inverted control (RPI#31312/31313). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs significantly reduce EGFR RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 14: RNAi mediated inhibition of PKC-alpha RNA expression

siNA constructs (**Table I**) are tested for efficacy in reducing PKC-alpha RNA expression in, for example in A549 cells. Cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

In a non-limiting example, siNA constructs were screened for activity (see **Figure 26**) and compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in **Figure 26**, the siNA constructs significantly reduce PKC-alpha RNA expression. Leads generated from such a screen are then further assayed. In a non-limiting example, siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps are assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides, in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control).

Example 15: RNAi mediated inhibition of Myc RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing Myc (c-Myc) RNA expression in 293T cells. 293T cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells were 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37°C for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells were lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and

the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 27**. A screen of siNA constructs was compared to untreated cells, scrambled siNA control constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, three of the siNA constructs (RPI 30993/31069; RPI 30995/31071; and RPI 30996/31072) significantly reduce c-Myc RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 16: RNAi mediated inhibition of BCL2 RNA expression

siNA constructs (**Table I**) are tested for efficacy in reducing BCL2 RNA expression in, for example, A549 cells. Cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs is determined.

In a non-limiting example, A549 cells were transfected with 0.25 ug/well of lipid complexed with 25 nM siNA. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#30998/31074) was tested along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-

terminal phosphorothioate internucleotide linkage (RPI#31368/31369), which was also compared to a matched chemistry inverted control (RPI#31370/31371) and a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine and 2'-deoxy-2'-fluoro purine nucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31372/31373) which was also compared to a matched chemistry inverted control (RPI#31374/31375). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in **Figure 28**, the siNA constructs significantly reduce BCL2 RNA expression compared to scrambled, untreated, and transfection controls. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 17: RNAi mediated inhibition of CHK-1 RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing CHK-1 RNA expression in A549 cells. A549 cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells were lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 29**. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31003/31079) and a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and in which the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31302/31303), were compared to a matched chemistry inverted control (RPI#31314/31325). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs significantly reduce CHK-1 RNA expression compared to appropriate controls. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 18: RNAi mediated inhibition of BACE RNA expression

siNA constructs (**Table I**) are tested for efficacy in reducing BACE RNA expression in, for example in A549 cells. Cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37°C for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

In a non-limiting example, siNA constructs were screened for activity (see **Figure 30**) and compared to untreated cells, scrambled siNA control constructs (Scram1 and

Scram2), and cells transfected with lipid alone (transfection control). As shown in **Figure 30**, the siNA constructs significantly reduce BACE RNA expression. Leads generated from such a screen are then further assayed. In a non-limiting example, siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps are assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides, in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control).

Example 19: RNAi mediated inhibition of cyclin D1 RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing cyclin D1 RNA expression in A549 cells. A549 cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells were lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 31**. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#30988/31064) was assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31300/3130), which was also compared to a matched chemistry inverted control (RPI#31312/31313). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs significantly reduce cyclin D1 RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 20: RNAi mediated inhibition of PTP-1B RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing PTP-1B RNA expression in A549 cells. A549 cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells were lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 32**. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31018/31094) was assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31306/31307), which was also compared to a matched chemistry inverted control (RPI#31318/31319). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs significantly reduce PTP-1B RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 21: RNAi mediated inhibition of ERG2 RNA expression

siNA constructs (**Table I**) are tested for efficacy in reducing ERG2 RNA expression in, for example in DLD1 cells. Cells are plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

In a non-limiting example, siNA constructs were screened for activity (see **Figure 33**) and compared to untreated cells, scrambled siNA control constructs (Scram1 and

Scram2), and cells transfected with lipid alone (transfection control). As shown in **Figure 33**, the siNA constructs significantly reduce of ERG2 RNA expression. Leads generated from such a screen are then further assayed. In a non-limiting example, siNA constructs comprising ribonucleotides and 3'-terminal dithymidine caps are assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides, in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity. These siNA constructs are compared to appropriate matched chemistry inverted controls. In addition, the siNA constructs are also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs, and cells transfected with lipid alone (transfection control). Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 22: RNAi mediated inhibition of PCNA RNA expression

siNA constructs (**Table I**) were tested for efficacy in reducing PCNA RNA expression in A549 cells. A549 cells were plated approximately 24h before transfection in 96-well plates at 5,000-7,500 cells/well, 100 µl/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs were mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 µl/well and incubated for 20 min. at room temperature. The siNA transfection mixtures were added to cells to give a final siNA concentration of 25 nM in a volume of 150 µl. Each siNA transfection mixture was added to 3 wells for triplicate siNA treatments. Cells were incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA was prepared from each well of treated cells. The supernatants with the transfection mixtures were first removed and discarded, then the cells were lysed and RNA prepared from each well. Target gene expression following treatment was evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data were averaged and the standard deviations determined for each treatment. Normalized data were graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs was determined.

Results of this study are shown in **Figure 34**. A siNA construct comprising ribonucleotides and 3'-terminal dithymidine caps (RPI#31035/31111) was assayed along with a chemically modified siNA construct comprising 2'-deoxy-2'-fluoro pyrimidine nucleotides and purine ribonucleotides in which the sense strand of the siNA is further modified with 5' and 3'-terminal inverted deoxyabasic caps and the antisense strand comprises a 3'-terminal phosphorothioate internucleotide linkage (RPI#31310/31311), which was also compared to a matched chemistry inverted control (RPI#31322/31323). In addition, the siNA constructs were also compared to untreated cells, cells transfected with lipid and scrambled siNA constructs (Scram1 and Scram2), and cells transfected with lipid alone (transfection control). As shown in the figure, both siNA constructs significant reduce PCNA RNA expression. Additional stabilization chemistries as described in **Table IV** are similarly assayed for activity.

Example 23: Indications

The siNA molecules of the invention can be used to treat a variety of diseases and conditions through modulation of gene expression. Using the methods described herein, chemically modified siNA molecules can be designed to modulate the expression any number of target genes, including but not limited to genes associated with cancer, metabolic diseases, infectious diseases such as viral, bacterial or fungal infections, neurologic diseases, musculoskeletal diseases, diseases of the immune system, diseases associated with signaling pathways and cellular messengers, and diseases associated with transport systems including molecular pumps and channels.

Non-limiting examples of various viral genes that can be targeted using siRNA molecules of the invention include Hepatitis C Virus (HCV, for example Genbank Accession Nos: D11168, D50483.1, L38318 and S82227), Hepatitis B Virus (HBV, for example GenBank Accession No. AF100308.1), Human Immunodeficiency Virus type 1 (HIV-1, for example GenBank Accession No. U51188), Human Immunodeficiency Virus type 2 (HIV-2, for example GenBank Accession No. X60667), West Nile Virus (WNV for example GenBank accession No. NC_001563), cytomegalovirus (CMV for example GenBank Accession No. NC_001347), respiratory syncytial virus (RSV for example GenBank Accession No. NC_001781), influenza virus (for example example GenBank Accession No. AF037412, rhinovirus (for example, GenBank accession numbers:

D00239, X02316, X01087, L24917, M16248, K02121, X01087), papillomavirus (for example GenBank Accession No. NC_001353), Herpes Simplex Virus (HSV for example GenBank Accession No. NC_001345), and other viruses such as HTLV (for example GenBank Accession No. AJ430458). Due to the high sequence variability of many viral genomes, selection of siRNA molecules for broad therapeutic applications would likely involve the conserved regions of the viral genome. Nonlimiting examples of conserved regions of the viral genomes include but are not limited to 5'-Non Coding Regions (NCR), 3'- Non Coding Regions (NCR) and/or internal ribosome entry sites (IRES). siRNA molecules designed against conserved regions of various viral genomes will enable efficient inhibition of viral replication in diverse patient populations and may ensure the effectiveness of the siRNA molecules against viral quasi species which evolve due to mutations in the non-conserved regions of the viral genome.

Non-limiting examples of human genes that can be targeted using siRNA molecules of the invention using methods described herein include any human RNA sequence, for example those commonly referred to by Genbank Accession Number. These RNA sequences can be used to design siRNA molecules that inhibit gene expression and therefore abrogate diseases, conditions, or infections associated with expression of those genes. Such non-limiting examples of human genes that can be targeted using siRNA molecules of the invention include VEGFr (VEGFr-1 for example GenBank Accession No. XM_067723, VEGFr-2 for example GenBank Accession No. AF063658), HER1, HER2, HER3, and HER4 (for example Genbank Accession Nos: NM_005228, NM_004448, NM_001982, and NM_005235 respectively), telomerase (TERT, for example GenBank Accession No. NM_003219), telomerase RNA (for example GenBank Accession No. U86046), NFkappaB, Rel-A (for example GenBank Accession No. NM_005228), NOGO (for example GenBank Accession No. AB020693), NOGOr (for example GenBank Accession No. XM_015620), RAS (for example GenBank Accession No. NM_004283), RAF (for example GenBank Accession No. XM_033884), CD20 (for example GenBank Accession No. X07203), METAP2 (for example GenBank Accession No. NM_003219), CLCA1 (for example GenBank Accession No. NM_001285) , phospholamban (for example GenBank Accession No. NM_002667), PTP1B (for example GenBank Accession No. M31724), and others, for example, those shown in Table III.

The siNA molecule of the invention can also be used in a variety of agricultural applications involving modulation of endogenous or exogenous gene expression in plants using siNA, including use as insecticidal, antiviral and anti-fungal agents or modulate plant traits such as oil and starch profiles and stress resistance.

Example 24: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes, siNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that cleave

only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms of target RNA) are used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches one skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Table I

Target	Target Pos	Target Sequence	Seq ID	strand	RPI#	Aliases	Sequence	SeqID #
ABCB1	118	CAUUCCUCCUGGAAAUUCAACCU	1	sense	30937	ABCB1:120U21 siRNA stab04	B uuccuccuGGAAAuucAAcTT B	186
ABCB1	618	UUCCUCUCAUGAUGCUGGUGUUU	2	sense	30938	ABCB1:620U21 siRNA stab04	B ccucucAuGAuGcuGGuGuTT B	187
ABCB1	1867	CACGAUAGCUGAAAACAUUCGCU	3	sense	30939	ABCB1:1869U21 siRNA stab04	B cGAuAGcuGAAAAcAuucGTT B	188
ABCB1	2334	AAAAUGCAGCUGAUGAAUCCAAA	4	sense	30940	ABCB1:2336U21 siRNA stab04	B AAuGcAGcuGAuGAAuccATT B	189
ABCB1	118	CAUUCCUCCUGGAAAUUCAACCU	1	antisense	30941	ABCB1:138L21 siRNA (120C) stab05	GuuGAAuuuccAGGAGGAATsT	190
ABCB1	618	UUCCUCUCAUGAUGCUGGUGUUU	2	antisense	30942	ABCB1:638L21 siRNA (620C) stab05	AcAccAGcAucAuGAGAGGTsT	191
ABCB1	1867	CACGAUAGCUGAAAACAUUCGCU	3	antisense	30943	ABCB1:1887L21 siRNA (1869C) stab05	cGAAuGuuuucAGcuAucGTsT	192
ABCB1	2334	AAAAUGCAGCUGAUGAAUCCAAA	4	antisense	30944	ABCB1:2354L21 siRNA (2336C) stab05	uGGAuucAucAGcuGcAuuTsT	193
ABCB1	118	CAUUCCUCCUGGAAAUUCAACCU	1	sense	31013	ABCB1:120U21 siRNA	UUCCUCCUGGAAAUUCAACTT	194
ABCB1	618	UUCCUCUCAUGAUGCUGGUGUUU	2	sense	31014	ABCB1:620U21 siRNA	CCUCUCAUGAUGCUGGUGUTT	195
ABCB1	1867	CACGAUAGCUGAAAACAUUCGCU	3	sense	31015	ABCB1:1869U21 siRNA	CGAUAGCUGAAAACAUUCGTT	196
ABCB1	2334	AAAAUGCAGCUGAUGAAUCCAAA	4	sense	31016	ABCB1:2336U21 siRNA	AAUGCAGCUGAUGAAUCCATT	197
ABCB1	118	CAUUCCUCCUGGAAAUUCAACCU	1	antisense	31089	ABCB1:138L21 siRNA (120C)	GUUGAAUUUCCAGGAGGAATT	198
ABCB1	618	UUCCUCUCAUGAUGCUGGUGUUU	2	antisense	31090	ABCB1:638L21 siRNA (620C)	ACACCAGCAUCAUGAGAGGTT	199
ABCB1	1867	CACGAUAGCUGAAAACAUUCGCU	3	antisense	31091	ABCB1:1887L21 siRNA (1869C)	CGAAUGUUUUCAGCUAUCGTT	200
ABCB1	2334	AAAAUGCAGCUGAUGAAUCCAAA	4	antisense	31092	ABCB1:2354L21 siRNA (2336C)	UGGAUUCAUCAGCUGCAUUTT	201
ADORA1	919	AGUUCGAGAAGGUCAUCAGCAUG	5	sense	30721	ADORA1:921U21 siRNA stab04	B uucGAGAAGGucAucAGcATT B	202
ADORA1	1621	GACCAGGUGUCUAGAGGCAACAG	6	sense	30722	ADORA1:1623U21 siRNA stab04	B ccAGGuGucuAGAGGcAAcTT B	203
ADORA1	1819	GGACCAAGCUUAAGGAGAGGAGA	7	sense	30723	ADORA1:1821U21 siRNA stab04	B AccAAGcuuAAGGAGAGGATT B	204
ADORA1	2773	GUCGGUUGACCUUCUGAACAUGA	8	sense	30724	ADORA1:2775U21 siRNA stab04	B cGGuuGAccuucuGAAcAuTT B	205
ADORA	919	AGUUCGAGAAGGUCAUCAGCAUG	5	antisense	30725	ADORA1:939L21 siRNA	uGcuGAuGAccuucucGAATsT	206

1						(921C) stab05		
ADORA 1	1621	GACCAGGUGUCUAGAGGCAACAG	6	antisense	30726	ADORA1:1641L21 siRNA (1623C) stab05	GuuGccucuAGAcAccuGGTsT	207
ADORA 1	1819	GGACCAAGCUUAAGGAGAGGAGA	7	antisense	30727	ADORA1:1839L21 siRNA (1821C) stab05	uccucuccuuAAGcuuGGuTsT	208
ADORA 1	2773	GUCGGUUGACCUUCUGAACAUGA	8	antisense	30728	ADORA1:2793L21 siRNA (2775C) stab05	AuGuucAGAAGGucAAccGTsT	209
ADORA 1	919	AGUUCGAGAAGGUCAUCAGCAUG	5	sense	31041	ADORA1:921U21 siRNA	UUCGAGAAGGUCAUCAGCATT	210
ADORA 1	1621	GACCAGGUGUCUAGAGGCAACAG	6	sense	31042	ADORA1:1623U21 siRNA	CCAGGUGUCUAGAGGCAACTT	211
ADORA 1	1819	GGACCAAGCUUAAGGAGAGGAGA	7	sense	31043	ADORA1:1821U21 siRNA	ACCAAGCUUAAGGAGAGGATT	212
ADORA 1	2773	GUCGGUUGACCUUCUGAACAUGA	8	sense	31044	ADORA1:2775U21 siRNA	CGGUUGACCUUCUGAACAUTT	213
ADORA 1	919	AGUUCGAGAAGGUCAUCAGCAUG	5	antisense	31117	ADORA1:939L21 siRNA (921C)	UGCUGAUGACCUUCUCGAATT	214
ADORA 1	1621	GACCAGGUGUCUAGAGGCAACAG	6	antisense	31118	ADORA1:1641L21 siRNA (1623C)	GUUGCCUCUAGACACCUGGTT	215
ADORA 1	1819	GGACCAAGCUUAAGGAGAGGAGA	7	antisense	31119	ADORA1:1839L21 siRNA (1821C)	UCCUCUCCUUAAGCUUGGUTT	216
ADORA 1	2773	GUCGGUUGACCUUCUGAACAUGA	8	antisense	31120	ADORA1:2793L21 siRNA (2775C)	AUGUUCAGAAGGUCAACCGTT	217
b2a2	283	UGACCAUCAAUAAGGAAGAAGCC	9	sense	31594	b2a2:283U21 siRNA	ACCAUCAAUAAGGAAGAAGTT	218
b2a2	286	CCAUCAAUAAGGAAGAAGCCCUU	10	sense	31595	b2a2:286U21 siRNA	AUCAAUAAGGAAGAAGCCCTT	219
b2a2	282	CUGACCAUCAAUAAGGAAGAAGC	11	sense	31596	b2a2:282U21 siRNA	GACCAUCAAUAAGGAAGAATT	220
b2a2	290	CAAUAAGGAAGAAGCCCUUCAGC	12	sense	31597	b2a2:290U21 siRNA	AUAAGGAAGAAGCCCUUCATT	221
b2a2	301	UGACCAUCAAUAAGGAAGAAGCC	9	antisense	31598	b2a2:301L21 siRNA (283C)	CUUCUUCCUUAUUGAUGGUTT	222
b2a2	304	CCAUCAAUAAGGAAGAAGCCCUU	10	antisense	31599	b2a2:304L21 siRNA (286C)	GGGCUUCUUCCUUAUUGAUTT	223
b2a2	300	CUGACCAUCAAUAAGGAAGAAGC	11	antisense	31600	b2a2:300L21 siRNA (282C)	UUCUUCCUUAUUGAUGGUCTT	224
b2a2	308	CAAUAAGGAAGAAGCCCUUCAGC	12	antisense	31601	b2a2:308L21 siRNA (290C)	UGAAGGGCUUCUUCCUUAUTT	225
b3a2	356	UGGAUUUAAGCAGAGUUCAAAAG	13	sense	31602	b3a2:356U21 siRNA	GAUUUAAGCAGAGUUCAAATT	226
b3a2	365	GCAGAGUUCAAAAGCCCUUCAGC	14	sense	31603	b3a2:365U21 siRNA	AGAGUUCAAAAGCCCUUCATT	227
b3a2	364	AGCAGAGUUCAAAAGCCCUUCAG	15	sense	31604	b3a2:364U21 siRNA	CAGAGUUCAAAAGCCCUUCTT	228
b3a2	357	GGAUUUAAGCAGAGUUCAAAAGC	16	sense	31605	b3a2:357U21 siRNA	AUUUAAGCAGAGUUCAAAATT	229
b3a2	374	UGGAUUUAAGCAGAGUUCAAAAG	13	antisense	31606	b3a2:374L21 siRNA (356C)	UUUGAACUCUGCUUAAAUCTT	230

b3a2	383	GCAGAGUUCAAAAGCCCUUCAGC	14	antisense	31607	b3a2:383L21 siRNA (365C)	UGAAGGGCUUUUGAACUCUTT	231
b3a2	382	AGCAGAGUUCAAAAGCCCUUCAG	15	antisense	31608	b3a2:382L21 siRNA (364C)	GAAGGGCUUUUGAACUCUGTT	232
b3a2	375	GGAUUUAAGCAGAGUUCAAAAGC	16	antisense	31609	b3a2:375L21 siRNA (357C)	UUUUGAACUCUGCUUAAAUTT	233
BACE	1490	AAUGGGUGAGGUUACCAACCAGU	17	sense	30729	BACE:1492U21 siRNA stab04	B uGGGuGAGGuuAccAAccATT B	234
BACE	1753	UCACCUUGGACAUGGAAGACUGU	18	sense	30730	BACE:1755U21 siRNA stab04	B AccuuGGAcAuGGAAGAcuTT B	235
BACE	3583	UAUGGGACCUGCUAAGUGUGGAA	19	sense	30732	BACE:3585U21 siRNA stab04	B uGGGAccuGcuAAGuGuGGTT B	236
BACE	1490	AAUGGGUGAGGUUACCAACCAGU	17	antisense	30733	BACE:1510L21 siRNA (1492C) stab05	uGGuuGGuAAccucAcccATsT	237
BACE	1753	UCACCUUGGACAUGGAAGACUGU	18	antisense	30734	BACE:1773L21 siRNA (1755C) stab05	AGucuuccAuGuccAAGGuTsT	238
BACE	3583	UAUGGGACCUGCUAAGUGUGGAA	19	antisense	30736	BACE:3603L21 siRNA (3585C) stab05	ccAcAcuuAGcAGGucccATsT	239
BACE	1490	AAUGGGUGAGGUUACCAACCAGU	17	sense	31005	BACE:1492U21 siRNA	UGGGUGAGGUUACCAACCATT	240
BACE	1753	UCACCUUGGACAUGGAAGACUGU	18	sense	31006	BACE:1755U21 siRNA	ACCUUGGACAUGGAAGACUTT	241
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	sense	31007	BACE:2459U21 siRNA	UAACAUUGGUGCAAAGAUUTT	242
BACE	3583	UAUGGGACCUGCUAAGUGUGGAA	19	sense	31008	BACE:3585U21 siRNA	UGGGACCUGCUAAGUGUGGTT	243
BACE	1490	AAUGGGUGAGGUUACCAACCAGU	17	antisense	31081	BACE:1510L21 siRNA (1492C)	UGGUUGGUAACCUCACCCATT	244
BACE	1753	UCACCUUGGACAUGGAAGACUGU	18	antisense	31082	BACE:1773L21 siRNA (1755C)	AGUCUUCCAUGUCCAAGGUTT	245
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	antisense	31083	BACE:2477L21 siRNA (2459C)	AAUCUUUGCACCAAUGUUATT	246
BACE	3583	UAUGGGACCUGCUAAGUGUGGAA	19	antisense	31084	BACE:3603L21 siRNA (3585C)	CCACACUUAGCAGGUCCCATT	247
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	sense	31378	BACE:2459U21 siRNA stab04	B uAAcAuuGGuGcAAAGAuuTT B	248
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	antisense	31381	BACE:2477L21 siRNA (2459C) stab05	AAucuuuGcAccAAuGuuATsT	249
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	sense	31384	BACE:2459U21 siRNA stab07	B u*AAcAuuGGuGcAAAGAuuTT* B	250
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	antisense	31387	BACE:2477L21 siRNA (2459C) stab11	*AAucuuuGcAccAAuGuuA*TsT	251
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	sense	31390	BACE:2459U21 siRNA inv stab04	B uuAGAAAcGuGGuuAcAAuTT B	252
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	antisense	31393	BACE:2477L21 siRNA (2459C) inv stab05	AuuGuAAccAcGuuucuAATsT	253

BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	sense	31396	BACE:2459U21 siRNA inv stab07	B uu*AGAAAcGuGGuuAcAAuTT* B	254
BACE	2457	CCUAACAUUGGUGCAAAGAUUGC	20	antisense	31399	BACE:2477L21 siRNA (2459C) inv stab11	*AuuGuAAccAcGuuucuAATsT*	255
BCL2	2098	UGGCUGUCUCUGAAGACUCUGCU	21	sense	30737	BCL2:2100U21 siRNA stab04	B GcuGucucuGAAGAcucuGTT B	256
BCL2	4426	CUUUACGUGGCCUGUUUCAACAC	22	sense	30739	BCL2:4428U21 siRNA stab04	B uuAcGuGGccuGuuucAAcTT B	257
BCL2	6231	AGUUUGGAUCAGGGAGUUGGAAG	23	sense	30740	BCL2:6233U21 siRNA stab04	B uuuGGAucAGGGAGuuGGATT B	258
BCL2	2098	UGGCUGUCUCUGAAGACUCUGCU	21	antisense	30741	BCL2:2118L21 siRNA (2100C) stab05	cAGAGucuucAGAGAcAGcTsT	259
BCL2	4426	CUUUACGUGGCCUGUUUCAACAC	22	antisense	30743	BCL2:4446L21 siRNA (4428C) stab05	GuuGAAAcAGGccAcGuAATsT	260
BCL2	6231	AGUUUGGAUCAGGGAGUUGGAAG	23	antisense	30744	BCL2:6251L21 siRNA (6233C) stab05	uccAAcucccuGAuccAAATsT	261
BCL2	2098	UGGCUGUCUCUGAAGACUCUGCU	21	sense	30997	BCL2:2100U21 siRNA	GCUGUCUCUGAAGACUCUGTT	262
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	sense	30998	BCL2:3222U21 siRNA	GGGAUGAUCAACAGGGUAGTT	263
BCL2	4426	CUUUACGUGGCCUGUUUCAACAC	22	sense	30999	BCL2:4428U21 siRNA	UUACGUGGCCUGUUUCAACTT	264
BCL2	6231	AGUUUGGAUCAGGGAGUUGGAAG	23	sense	31000	BCL2:6233U21 siRNA	UUUGGAUCAGGGAGUUGGATT	265
BCL2	2098	UGGCUGUCUCUGAAGACUCUGCU	21	antisense	31073	BCL2:2118L21 siRNA (2100C)	CAGAGUCUUCAGAGACAGCTT	266
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	antisense	31074	BCL2:3240L21 siRNA (3222C)	CUACCCUGUUGAUCAUCCCTT	267
BCL2	4426	CUUUACGUGGCCUGUUUCAACAC	22	antisense	31075	BCL2:4446L21 siRNA (4428C)	GUUGAAACAGGCCACGUAATT	268
BCL2	6231	AGUUUGGAUCAGGGAGUUGGAAG	23	antisense	31076	BCL2:6251L21 siRNA (6233C)	UCCAACUCCCUGAUCCAAATT	269
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	sense	31368	BCL2:3222U21 siRNA stab04	B GGGAuGAucAAcAGGGuAGTT B	270
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	antisense	31369	BCL2:3240L21 siRNA (3222C) stab05	cuAcccuGuuGAucAucccTsT	271
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	sense	31370	BCL2:3222U21 siRNA inv stab04	B GAuGGGAcAAcuAGuAGGGTT B	272
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	antisense	31371	BCL2:3240L21 siRNA (3222C) inv stab05	cccuAcuAGuuGucccAucTsT	273
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	sense	31372	BCL2:3222U21 siRNA stab07	B *GGGAuGAucAAcAGGGuAGTT* B	274
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	antisense	31373	BCL2:3240L21 siRNA (3222C) stab11	cu*AcccuGuuGAucAucccTsT*	275
BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	sense	31374	BCL2:3222U21 siRNA inv stab07	B *GAuGGGAcAAcuAGuAGGGTT* B	276

BCL2	3220	CAGGGAUGAUCAACAGGGUAGUG	24	antisense	31375	BCL2:3240L21 siRNA (3222C) inv stab11	cccuAcuAGuuGucccAucTsT	277
CCND1	1628	GCUGUAGUGGGGUUCUAGGCAUC	25	sense	30746	CCND1:1628U21 siRNA stab04	B uGuAGuGGGGuucuAGGcATT B	278
CCND1	2617	ACACACAAACCUUCUGCCUUUGA	26	sense	30747	CCND1:2617U21 siRNA stab04	B AcAcAAAccuucuGccuuuTT B	279
CCND1	3124	UCACAUUGUUUGCUGCUAUUGGA	27	sense	30748	CCND1:3124U21 siRNA stab04	B AcAuuGuuuGcuGcuAuuGTT B	280
CCND1	1646	GCUGUAGUGGGGUUCUAGGCAUC	25	antisense	30750	CCND1:1646L21 siRNA (1628C) stab05	uGccuAGAAccccAcuAcATsT	281
CCND1	2635	ACACACAAACCUUCUGCCUUUGA	26	antisense	30751	CCND1:2635L21 siRNA (2617C) stab05	AAAGGcAGAAGGuuuGuGuTsT	282
CCND1	3142	UCACAUUGUUUGCUGCUAUUGGA	27	antisense	30752	CCND1:3142L21 siRNA (3124C) stab05	cAAuAGcAGcAAAcAAuGuTsT	283
CCND1	695	GAACACUUCCUCUCCAAAAUGCC	28	sense	31009	CCND1:695U21 siRNA	ACACUUCCUCUCCAAAAUGTT	284
CCND1	1628	GCUGUAGUGGGGUUCUAGGCAUC	25	sense	31010	CCND1:1628U21 siRNA	UGUAGUGGGGUUCUAGGCATT	285
CCND1	2617	ACACACAAACCUUCUGCCUUUGA	26	sense	31011	CCND1:2617U21 siRNA	ACACAAACCUUCUGCCUUUTT	286
CCND1	3124	UCACAUUGUUUGCUGCUAUUGGA	27	sense	31012	CCND1:3124U21 siRNA	ACAUUGUUUGCUGCUAUUGTT	287
CCND1	713	GAACACUUCCUCUCCAAAAUGCC	28	antisense	31085	CCND1:713L21 siRNA (695C)	CAUUUUGGAGAGGAAGUGUTT	288
CCND1	1646	GCUGUAGUGGGGUUCUAGGCAUC	25	antisense	31086	CCND1:1646L21 siRNA (1628C)	UGCCUAGAACCCCACUACATT	289
CCND1	2635	ACACACAAACCUUCUGCCUUUGA	26	antisense	31087	CCND1:2635L21 siRNA (2617C)	AAAGGCAGAAGGUUUGUGUTT	290
CCND1	3142	UCACAUUGUUUGCUGCUAUUGGA	27	antisense	31088	CCND1:3142L21 siRNA (3124C)	CAAUAGCAGCAAACAAUGUTT	291
CCND1	695	GAACACUUCCUCUCCAAAAUGCC	28	sense	31304	CCND1:695U21 siRNA stab04	B AcAcuuccucuccAAAAuGTT B	292
CCND1	695	GAACACUUCCUCUCCAAAAUGCC	28	sense	31304	CCND1:695U21 siRNA stab04	B AcAcuuccucuccAAAAuGTT B	292
CCND1	695	GAACACUUCCUCUCCAAAAUGCC	28	sense	31304	CCND1:695U21 siRNA stab04	B AcAcuuccucuccAAAAuGTT B	292
CCND1	713	GAACACUUCCUCUCCAAAAUGCC	28	antisense	31305	CCND1:713L21 siRNA (695C) stab05	cAuuuuGGAGAGGAAGuGuTsT	293
CCND1	713	GAACACUUCCUCUCCAAAAUGCC	28	antisense	31305	CCND1:713L21 siRNA (695C) stab05	cAuuuuGGAGAGGAAGuGuTsT	293
CCND1	695	GAACACUUCCUCUCCAAAAUGCC	28	sense	31316	CCND1:695U21 siRNA inv stab04	B GuAAAAccucuccuucAcATT B	294
CCND1	713	GAACACUUCCUCUCCAAAAUGCC	28	antisense	31317	CCND1:713L21 siRNA (695C) inv stab05	uGuGAAGGAGAGGuuuuAcTsT	295
CDK2	344	CUGGACACUGAGACUGAGGGUGU	29	sense	31565	CDK2:344U21 siRNA	GGACACUGAGACUGAGGGUTT	296

CDK2	654	CCAUCAAGCUAGCAGACUUUGGA	30	sense	31566	CDK2:654U21 siRNA	AUCAAGCUAGCAGACUUUGTT	297
CDK2	1245	CACUCACCUUCUAGUCUUGGCCA	31	sense	31567	CDK2:1245U21 siRNA	CUCACCUUCUAGUCUUGGCTT	298
CDK2	1428	ACACGUUAGAUUUGCCGUACCAA	32	sense	31568	CDK2:1428U21 siRNA	ACGUUAGAUUUGCCGUACCTT	299
CDK2	362	CUGGACACUGAGACUGAGGGUGU	29	antisense	31569	CDK2:362L21 siRNA (344C)	ACCCUCAGUCUCAGUGUCCTT	300
CDK2	672	CCAUCAAGCUAGCAGACUUUGGA	30	antisense	31570	CDK2:672L21 siRNA (654C)	CAAAGUCUGCUAGCUUGAUTT	301
CDK2	1263	CACUCACCUUCUAGUCUUGGCCA	31	antisense	31571	CDK2:1263L21 siRNA (1245C)	GCCAAGACUAGAAGGUGAGTT	302
CDK2	1446	ACACGUUAGAUUUGCCGUACCAA	32	antisense	31572	CDK2:1446L21 siRNA (1428C)	GGUACGGCAAAUCUAACGUTT	303
CHEK1	369	UAUGGUCACAGGAGAGAAGGCAA	33	sense	30753	CHEK1:371U21 siRNA stab04	B uGGucAcAGGAGAGAAGGcTT B	304
CHEK1	1349	UGAGAAGUUGGGCUAUCAAUGGA	34	sense	30754	CHEK1:1351U21 siRNA stab04	B AGAAGuuGGGcuAucAAuGTT B	305
CHEK1	1878	GUUUCAGGGGACAUGAGUUUUCC	35	sense	30756	CHEK1:1880U21 siRNA stab04	B uucAGGGGAcAuGAGuuuuTT B	306
CHEK1	369	UAUGGUCACAGGAGAGAAGGCAA	33	antisense	30757	CHEK1:389L21 siRNA (371C) stab05	GccuucucuccuGuGAccATsT	307
CHEK1	1349	UGAGAAGUUGGGCUAUCAAUGGA	34	antisense	30758	CHEK1:1369L21 siRNA (1351C) stab05	cAuuGAuAGcccAAcuucuTsT	308
CHEK1	1878	GUUUCAGGGGACAUGAGUUUUCC	35	antisense	30760	CHEK1:1898L21 siRNA (1880C) stab05	AAAAcucAuGuccccuGAATsT	309
CHEK1	369	UAUGGUCACAGGAGAGAAGGCAA	33	sense	31001	CHEK1:371U21 siRNA	UGGUCACAGGAGAGAAGGCTT	310
CHEK1	1349	UGAGAAGUUGGGCUAUCAAUGGA	34	sense	31002	CHEK1:1351U21 siRNA	AGAAGUUGGGCUAUCAAUGTT	311
CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	sense	31003	CHEK1:1492U21 siRNA	AGGGUGAUGGAUUGGAGUUTT	312
CHEK1	1878	GUUUCAGGGGACAUGAGUUUUCC	35	sense	31004	CHEK1:1880U21 siRNA	UUCAGGGGACAUGAGUUUUTT	313
CHEK1	369	UAUGGUCACAGGAGAGAAGGCAA	33	antisense	31077	CHEK1:389L21 siRNA (371C)	GCCUUCUCUCCUGUGACCATT	314
CHEK1	1349	UGAGAAGUUGGGCUAUCAAUGGA	34	antisense	31078	CHEK1:1369L21 siRNA (1351C)	CAUUGAUAGCCCAACUUCUTT	315
CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	antisense	31079	CHEK1:1510L21 siRNA (1492C)	AACUCCAAUCCAUCACCCUTT	316
CHEK1	1878	GUUUCAGGGGACAUGAGUUUUCC	35	antisense	31080	CHEK1:1898L21 siRNA (1880C)	AAAACUCAUGUCCCCUGAATT	317
CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	sense	31302	CHEK1:1492U21 siRNA stab04	B AGGGuGAuGGAuuGGAGuuTT B	318
CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	antisense	31303	CHEK1:1510L21 siRNA (1492C) stab05	AAcuccAAuccAucAcccuTsT	319
CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	sense	31314	CHEK1:1492U21 siRNA inv stab04	B uuGAGGuuAGGuAGuGGGATT B	320

CHEK1	1490	UAAGGGUGAUGGAUUGGAGUUCA	36	antisense	31315	CHEK1:1510L21 siRNA (1492C) inv stab05	ucccAcuAccuAAccucAATsT	321
EGFR	3828	UAACCUCGUACUGGUGCCU	37	sense	25227	RPI 21550 EGFR 3830L23 AS as siRNA Str 1 (sense)	B UAACCUCGUACUGGUGCCUCC B	322
EGFR		ACCUCGUACUGGUGCCUCC	38	antisense	25228	RPI 21550 EGFR 3830L23 AS as siRNA Str 2 (antisense)	B GGAGGCACCAGUACGAGGUUA B	323
EGFR		AUUGGGGAUCUUGGAGUUU	39	antisense	25229	RPI 21549 EGFR as siRNA Str 2 (antisense)	B AAACUCCAAGAUCCCCAAUCA B	324
EGFR		UGAUUGGGGAUCUUGGAGU	40	sense	25230	RPI 21549 EGFR 3 as siRNA Str 1 (sense)	B UGAUUGGGGAUCUUGGAGUUU B	325
EGFR		GAAAUCACAGGGUUUUUGC	41	antisense	25233	RPI 21545 EGFR as siRNA Str 2 (antisense)	B GCAAAAACCCUGUGAUUUCCU B	326
EGFR		AGGAAAUCACAGGGUUUUU	42	sense	25234	RPI 21545 EGFR as siRNA Str 1 (sense)	B AGGAAAUCACAGGGUUUUUGC B	327
EGFR		ACUGCCAGAAACUGACCAA	43	antisense	25235	RPI 21543 EGFR as siRNA Str 2 (antisense)	B UUGGUCAGUUUCUGGCAGUUC B	328
EGFR		GAACUGCCAGAAACUGACC	44	sense	25236	RPI 21543 EGFR as siRNA Str 1 (sense)	B GAACUGCCAGAAACUGACCAA B	329
EGFR	3828	ACCUCGUACUGGUGCCUCC	38	sense	25249	RPI 21550 EGFR 3830L23 AS as siRNA Str 1 (sense) Inverted Control	B CCUCCGUGGUCAUGCUCCAAU B	330
EGFR	3828	AGGCACCAGUACGAGGUUA	45	sense	25250	RPI 21550 EGFR 3830L23 AS as siRNA Str 1 (sense) Inverted Control Compliment	B AUUGGAGCAUGACCACGGAGG B	331
EGFR	3828	UAACCUCGUACUGGUGCCU	37	sense	25804	RPI 21550 EGFR 3830L23 AS as siRNA Str 1 (sense) +2U overhang	UAACCUCGUACUGGUGCCUCCUU	332
EGFR		ACCUCGUACUGGUGCCUCC	38	antisense	25805	RPI 21550 EGFR 3830L23 AS as siRNA Str 2 (antisense) +2U overhang	GGAGGCACCAGUACGAGGUUAUU	333
EGFR		AUUGGGGAUCUUGGAGUUU	39	antisense	25806	RPI 21549 EGFR as siRNA Str 2 (antisense)+ 2U overhang	AAACUCCAAGAUCCCCAAUCAUU	334
EGFR		UGAUUGGGGAUCUUGGAGU	40	sense	25807	RPI 21549 EGFR 3 as siRNA Str 1 (sense)+2U overhang	UGAUUGGGGAUCUUGGAGUUUUU	335
EGFR		GAAAUCACAGGGUUUUUGC	41	antisense	25810	RPI 21545 EGFR as siRNA Str 2	GCAAAAACCCUGUGAUUUCCUUU	336

						(antisense)+2U overhang		
EGFR		AGGAAAUCACAGGGUUUUU	42	sense	25811	RPI 21545 EGFR as siRNA Str 1 (sense)+2U overhang	AGGAAAUCACAGGGUUUUUGCUU	337
EGFR		ACUGCCAGAAACUGACCAA	43	antisense	25812	RPI 21543 EGFR as siRNA Str 2 (antisense)+2U overhang	UUGGUCAGUUUCUGGCAGUUCUU	338
EGFR		GAACUGCCAGAAACUGACC	44	sense	25813	RPI 21543 EGFR as siRNA Str 1 (sense)+2U overhang	GAACUGCCAGAAACUGACCAAUU	339
EGFR	3828	UAACCUCGUACUGGUGCCU	37	sense	25824	RPI 21550 EGFR 3830L23 AS as siRNA Str 1 (sense) +2U overhang	B UAACCUCGUACUGGUGCCUCCUU B	340
EGFR		ACCUCGUACUGGUGCCUCC	38	antisense	25825	RPI 21550 EGFR 3830L23 AS as siRNA Str 2 (antisense) +2U overhang	B GGAGGCACCAGUACGAGGUUAUU B	341
EGFR		AUUGGGGAUCUUGGAGUUU	39	antisense	25826	RPI 21549 EGFR as siRNA Str 2 (antisense)+ 2U overhang	B AAACUCCAAGAUCCCCAAUCAUU B	342
EGFR		UGAUUGGGGAUCUUGGAGU	40	sense	25827	RPI 21549 EGFR 3 as siRNA Str 1 (sense)+2U overhang	B UGAUUGGGGAUCUUGGAGUUUUU B	343
EGFR		GAAAUCACAGGGUUUUUGC	41	antisense	25830	RPI 21545 EGFR as siRNA Str 2 (antisense)+2U overhang	B GCAAAAACCCUGUGAUUUCCUUU B	344
EGFR		AGGAAAUCACAGGGUUUUU	42	sense	25831	RPI 21545 EGFR as siRNA Str 1 (sense)+2U overhang	B AGGAAAUCACAGGGUUUUUGCUU B	345
EGFR		ACUGCCAGAAACUGACCAA	43	antisense	25832	RPI 21543 EGFR as siRNA Str 2 (antisense)+2U overhang	B UUGGUCAGUUUCUGGCAGUUCUU B	346
EGFR		GAACUGCCAGAAACUGACC	44	sense	25833	RPI 21543 EGFR as siRNA Str 1 (sense)+2U overhang	B GAACUGCCAGAAACUGACCAAUU B	347
EGFR	799	GAACUGCCAGAAACUGACC	44	sense	30705	EGFR:801U21 siRNA stab04	B GAAcuGccAGAAAcuGAccTT B	348
EGFR	1380	AGGAAAUCACAGGGUUUUU	42	sense	30706	EGFR:1382U21 siRNA stab04	B AGGAAAucAcAGGGuuuuuTT B	349
EGFR	3064	GUUCCGUGAGUUGAUCAUC	46	sense	30707	EGFR:3066U21 siRNA stab04	B GuuccGuGAGuuGAucAucTT B	350
EGFR	3152	CCAAGUCCUACAGACUCCA	47	sense	30708	EGFR:3154U21 siRNA	B ccAAGuccuAcAGAcuccATT B	351

						stab04		
EGFR	799	GAACUGCCAGAAACUGACC	44	antisense	30709	EGFR:819L21 siRNA (801C) stab05	GGucAGuuucuGGcAGuucTsT	352
EGFR	1380	AGGAAAUCACAGGGUUUUU	42	antisense	30710	EGFR:1400L21 siRNA (1382C) stab05	AAAAAcccuGuGAuuuccuTsT	353
EGFR	3064	GUUCCGUGAGUUGAUCAUC	46	antisense	30711	EGFR:3084L21 siRNA (3066C) stab05	GAuGAucAAcucAcGGAAcTsT	354
EGFR	3152	CCAAGUCCUACAGACUCCA	47	antisense	30712	EGFR:3172L21 siRNA (3154C) stab05	uGGAGucuGuAGGAcuuGGTsT	355
EGFR	799	GAACUGCCAGAAACUGACC	44	sense	30985	EGFR:801U21 siRNA	GAACUGCCAGAAACUGACCTT	356
EGFR	1380	AGGAAAUCACAGGGUUUUU	42	sense	30986	EGFR:1382U21 siRNA	AGGAAAUCACAGGGUUUUUTT	357
EGFR	3064	GUUCCGUGAGUUGAUCAUC	46	sense	30987	EGFR:3066U21 siRNA	GUUCCGUGAGUUGAUCAUCTT	358
EGFR	3152	CCAAGUCCUACAGACUCCA	47	sense	30988	EGFR:3154U21 siRNA	CCAAGUCCUACAGACUCCATT	359
EGFR	799	GAACUGCCAGAAACUGACC	44	antisense	31061	EGFR:819L21 siRNA (801C)	GGUCAGUUUCUGGCAGUUCTT	360
EGFR	1380	AGGAAAUCACAGGGUUUUU	42	antisense	31062	EGFR:1400L21 siRNA (1382C)	AAAAACCCUGUGAUUUCCUTT	361
EGFR	3064	GUUCCGUGAGUUGAUCAUC	46	antisense	31063	EGFR:3084L21 siRNA (3066C)	GAUGAUCAACUCACGGAACTT	362
EGFR	3152	CCAAGUCCUACAGACUCCA	47	antisense	31064	EGFR:3172L21 siRNA (3154C)	UGGAGUCUGUAGGACUUGGTT	363
EGFR	3152	CCAAGUCCUACAGACUCCA	47	sense	31300	EGFR:3154U21 siRNA stab04	B ccAAGuccuAcAGAcuccATT B	351
EGFR	3152	CCAAGUCCUACAGACUCCA	47	antisense	31301	EGFR:3172L21 siRNA (3154C) stab05	uGGAGucuGuAGGAcuuGGTsT	355
EGFR	3152	CCAAGUCCUACAGACUCCA	47	sense	31312	EGFR:3154U21 siRNA inv stab04	B AccucAGAcAuccuGAAccTT B	364
EGFR	3152	CCAAGUCCUACAGACUCCA	47	antisense	31313	EGFR:3172L21 siRNA (3154C) inv stab05	GGuucAGGAuGucuGAGGuTsT	365
ERG2	242	AGGUGAAUGGCUCAAGGAACUCU	48	sense	30761	ERG2:244U21 siRNA stab04	B GuGAAuGGcucAAGGAAcuTT B	366
ERG2	517	AAGGAACUGUGCAAGAUGACCAA	49	sense	30762	ERG2:519U21 siRNA stab04	B GGAAcuGuGcAAGAuGAccTT B	367
ERG2	759	GAAAGCUGCUCAACCAUCUCCUU	50	sense	30763	ERG2:761U21 siRNA stab04	B AAGcuGcucAAccAucuccTT B	368
ERG2	767	CUCAACCAUCUCCUUCCACAGUG	51	sense	30764	ERG2:769U21 siRNA stab04	B cAAccAucuccuuccAcAGTT B	369
ERG2	242	AGGUGAAUGGCUCAAGGAACUCU	48	antisense	30765	ERG2:262L21 siRNA (244C) stab05	AGuuccuuGAGccAuucAcTsT	370
ERG2	517	AAGGAACUGUGCAAGAUGACCAA	49	antisense	30766	ERG2:537L21 siRNA (519C) stab05	GGucAucuuGcAcAGuuccTsT	371

ERG2	759	GAAAGCUGCUCAACCAUCUCCUU	50	antisense	30767	ERG2:779L21 siRNA (761C) stab05	GGAGAuGGuuGAGcAGcuuTsT	372
ERG2	767	CUCAACCAUCUCCUUCCACAGUG	51	antisense	30768	ERG2:787L21 siRNA (769C) stab05	cuGuGGAAGGAGAuGGuuGTsT	373
ERG2	242	AGGUGAAUGGCUCAAGGAACUCU	48	sense	31045	ERG2:244U21 siRNA	GUGAAUGGCUCAAGGAACUTT	374
ERG2	517	AAGGAACUGUGCAAGAUGACCAA	49	sense	31046	ERG2:519U21 siRNA	GGAACUGUGCAAGAUGACCTT	375
ERG2	759	GAAAGCUGCUCAACCAUCUCCUU	50	sense	31047	ERG2:761U21 siRNA	AAGCUGCUCAACCAUCUCCTT	376
ERG2	767	CUCAACCAUCUCCUUCCACAGUG	51	sense	31048	ERG2:769U21 siRNA	CAACCAUCUCCUUCCACAGTT	377
ERG2	242	AGGUGAAUGGCUCAAGGAACUCU	48	antisense	31121	ERG2:262L21 siRNA (244C)	AGUUCCUUGAGCCAUUCACTT	378
ERG2	517	AAGGAACUGUGCAAGAUGACCAA	49	antisense	31122	ERG2:537L21 siRNA (519C)	GGUCAUCUUGCACAGUUCCTT	379
ERG2	759	GAAAGCUGCUCAACCAUCUCCUU	50	antisense	31123	ERG2:779L21 siRNA (761C)	GGAGAUGGUUGAGCAGCUUTT	380
ERG2	767	CUCAACCAUCUCCUUCCACAGUG	51	antisense	31124	ERG2:787L21 siRNA (769C)	CUGUGGAAGGAGAUGGUUGTT	381
EZH2	201	UACAUGCGACUGAGACAGCUCAA	52	sense	31416	EZH2:203U21 siRNA	CAUGCGACUGAGACAGCUCTT	382
EZH2	338	GCACAUCCUGACUUCUGUGAGCU	53	sense	31417	EZH2:340U21 siRNA	ACAUCCUGACUUCUGUGAGTT	383
EZH2	688	ACGAUGAUGAUGAUGGAGACGAU	54	sense	31418	EZH2:690U21 siRNA	GAUGAUGAUGAUGGAGACGTT	384
EZH2	1493	UGACAAUUUCUGUGCCAUUGCUA	55	sense	31419	EZH2:1495U21 siRNA	ACAAUUUCUGUGCCAUUGCTT	385
EZH2	201	UACAUGCGACUGAGACAGCUCAA	52	antisense	31420	EZH2:221L21 siRNA (203C)	GAGCUGUCUCAGUCGCAUGTT	386
EZH2	338	GCACAUCCUGACUUCUGUGAGCU	53	antisense	31421	EZH2:358L21 siRNA (340C)	CUCACAGAAGUCAGGAUGUTT	387
EZH2	688	ACGAUGAUGAUGAUGGAGACGAU	54	antisense	31422	EZH2:708L21 siRNA (690C)	CGUCUCCAUCAUCAUCAUCTT	388
EZH2	1493	UGACAAUUUCUGUGCCAUUGCUA	55	antisense	31423	EZH2:1513L21 siRNA (1495C)	GCAAUGGCACAGAAAUUGUTT	389
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	29694	FLT1:349U21 siRNA stab01	CsUsGsAsGsUUUAAAAGGCACCCTsT	390
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	29695	FLT1:2340U21 siRNA stab01	CsAsAsCsCsACAAAAUACAACAATsT	391
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	29696	FLT1:3912U21 siRNA stab01	CsCsUsGsGsAAAGAAUCAAAACCTsT	392
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	29697	FLT1:2949U21 siRNA stab01	GsCsAsAsGsGAGGGCCUCUGAUGTsT	393
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	29698	FLT1:369L21 siRNA (349C) stab01	GsGsGsUsGsCCUUUUAAACUCAGTsT	394
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29699	FLT1:2358L21 siRNA (2340C) stab01	UsUsGsUsUsGUAUUUUGUGGUUGTsT	395
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	29700	FLT1:3932L21 siRNA	GsGsUsUsUsUGAUUCUUUCCAGGTsT	396

WO 03/074654 PCT/US03/05028

						(3912C) stab01		
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	29701	FLT1:2969L21 siRNA (2949C) stab01	CsAsUsCsAsGAGGCCCUCCUUGCTsT	397
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	29702	FLT1:349U21 siRNA stab03	csusGsAsGuuuAAAAGGcAcscscsTsT	398
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	29703	FLT1:2340U21 siRNA stab03	csAsAscscAcAAAAuAcAAcsAsAsTsT	399
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	29704	FLT1:3912U21 siRNA stab03	cscsusGsGAAAGAAucAAAAscscsTsT	400
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	29705	FLT1:2949U21 siRNA stab03	GscsAsAsGGAGGGccucuGAsusGsTsT	401
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	29706	FLT1:369L21 siRNA (349C) stab02	GsGsGsUsGsCsCsUsUsUsUsAsAsAsCsUsCsAsGsTsT	402
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29707	FLT1:2358L21 siRNA (2340C) stab02	UsUsGsUsUsGsUsAsUsUsUsUsGsUsGsGsUsUsGsTsT	403
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	29708	FLT1:3932L21 siRNA (3912C) stab02	GsGsUsUsUsUsGsAsUsUsCsUsUsUsCsCsAsGsGsTsT	404
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	29709	FLT1:2969L21 siRNA (2949C) stab02	CsAsUsCsAsGsAsGsGsCsCsCsUsCsCsUsUsGsCsTsT	405
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	29981	FLT1:2340U21 siRNA Native	CAACCACAAAAUACAACAAGA	406
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29982	FLT1:2358L21 siRNA (2340C) Native	UUGUUGUAUUUUGUGGUUGUU	407
FLT1	2340	AACAACCACAAAAUACAACAAGA	57	sense	29983	FLT1:2342U21 siRNA stab01 inv	AsAsCsAsAsCAUAAAACACCAACTsT	408
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29984	FLT1:2358L21 siRNA (2340C) stab01 inv	GsUsUsGsGsUGUUUUAUGUUGUUTsT	409
FLT1	2340	AACAACCACAAAAUACAACAAGA	57	sense	29985	FLT1:2342U21 siRNA stab03 inv	AsAscsAsAcAuAAAAcAccAsAscsTsT	410
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29986	FLT1:2358L21 siRNA (2340C) stab02 inv	GsUsUsGsGsUsGsUsUsUsAsUsGsUsUsGsUsUsTsT	411
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	29987	FLT1:2340U21 siRNA inv Native	AGAACAACAUAAAACACCAAC	412
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	29988	FLT1:2358L21 siRNA (2340C) inv Native	UUGUUGGUGUUUUAUGUUGUU	413
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30075	FLT1:2340U21 siRNA	CAACCACAAAAUACAACAATT	414
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30076	FLT1:2358L21 siRNA (2340C)	UUGUUGUAUUUUGUGGUUGTT	415
FLT1	2340	AACAACCACAAAAUACAACAAGA	57	sense	30077	FLT1:2342U21 siRNA inv	AGAACAACAUAAAACACCATT	416
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30078	FLT1:2358L21 siRNA (2340C) inv	UUGUUGGUGUUUUAUGUUGTT	417
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30187	FLT1:2358L21 siRNA	uuGuuGuAuuuuGuGGuuGTT	418

						(2340C) 2'-F U,C		
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30190	FLT1:2358L21 siRNA (2340C) nitroindole	uuGuuGuAuuuuGuGGuuGXX	419
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30193	FLT1:2358L21 siRNA (2340C) nitropyrole	uuGuuGuAuuuuGuGGuuGZZ	420
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30196	FLT1:2340U21 siRNA sense iB caps w/2'FY's	B cAAccAcAAAAuAcAAcAATT B	421
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30199	FLT1:2340U21 siRNA sense iB caps	cAAccAcAAAAuAcAAcAATT	422
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30340	FLT1:2358L21 siRNA (2340C) 3'dT	uuGuuGuAuuuuGuGGuuGTX	423
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30341	FLT1:2358L21 siRNA (2340C) glyceryl	uuGuuGuAuuuuGuGGuuGTX	424
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30342	FLT1:2358L21 siRNA (2340C) 3'OMeU	uuGuuGuAuuuuGuGGuuGTU	425
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30343	FLT1:2358L21 siRNA (2340C) L-dT	uuGuuGuAuuuuGuGGuuGTt	426
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30344	FLT1:2358L21 siRNA (2340C) L-rU	uuGuuGuAuuuuGuGGuuGTu	427
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30345	FLT1:2358L21 siRNA (2340C) idT	uuGuuGuAuuuuGuGGuuGTD	428
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30346	FLT1:2358L21 siRNA (2340C) 3'dT	uuGuuGuAuuuuGuGGuuGXT	429
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30416	FLT1:2358L21 siRNA (2340C) TsT	uuGuuGuAuuuuGuGGuuGTsT	430
FLT1	1182	UCGUGUAAGGAGUGGACCAUCAU	60	sense	30777	FLT1:1184U21 siRNA stab04	B GuGuAAGGAGuGGAccAucTT B	431
FLT1	3501	UUACGGAGUAUUGCUGUGGGAAA	61	sense	30778	FLT1:3503U21 siRNA stab04	B AcGGAGuAuuGcuGuGGGATT B	432
FLT1	4713	UAGCAGGCCUAAGACAUGUGAGG	62	sense	30779	FLT1:4715U21 siRNA stab04	B GcAGGccuAAGAcAuGuGATT B	433
FLT1	4751	AGCAAAAAGCAAGGGAGAAAAGA	63	sense	30780	FLT1:4753U21 siRNA stab04	B cAAAAAGcAAGGGAGAAAATT B	434
FLT1	1182	UCGUGUAAGGAGUGGACCAUCAU	60	antisense	30781	FLT1:1202L21 siRNA (1184C) stab05	GAuGGuccAcuccuuAcAcTsT	435
FLT1	3501	UUACGGAGUAUUGCUGUGGGAAA	61	antisense	30782	FLT1:3521L21 siRNA (3503C) stab05	ucccAcAGcAAuAcuccGuTsT	436
FLT1	4713	UAGCAGGCCUAAGACAUGUGAGG	62	antisense	30783	FLT1:4733L21 siRNA (4715C) stab05	ucAcAuGucuuAGGccuGcTsT	437
FLT1	4751	AGCAAAAAGCAAGGGAGAAAAGA	63	antisense	30784	FLT1:4771L21 siRNA (4753C) stab05	uuuucucccuuGcuuuuuGTsT	438
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30955	FLT1:2340U21 siRNA	B cAAccAcAAAAuAcAAcAATT B	439

						stab07		
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30956	FLT1:2358L21 siRNA (2340C) stab08	uuGuuGuAuuuuGuGGuuGTsT	440
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30963	FLT1:2340U21 siRNA inv	AACAACAUAAAACACCAACTT	441
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30964	FLT1:2358L21 siRNA (2340C) inv	GUUGGUGUUUUAUGUUGUUTT	442
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30965	FLT1:2340U21 siRNA stab04 inv	B AAcAAcAuAAAAcAccAAcTT B	443
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30966	FLT1:2358L21 siRNA (2340C) stab05 inv	GuuGGuGuuuuAuGuuGuuTsT	444
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	30967	FLT1:2340U21 siRNA stab07 inv	B *AAcAAcAuAAAAcAccAAcTT* B	445
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	30968	FLT1:2358L21 siRNA (2340C) stab08 inv	GuuGGuGuuuuAuGuuGuuTsT	446
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31182	FLT1:349U21 siRNA TT	CUGAGUUUAAAAGGCACCCTT	447
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31183	FLT1:2949U21 siRNA TT	GCAAGGAGGGCCUCUGAUGTT	448
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31184	FLT1:3912U21 siRNA TT	CCUGGAAAGAAUCAAAACCTT	449
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31185	FLT1:367L21 siRNA (349C) TT	GGGUGCCUUUUAAACUCAGTT	450
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31186	FLT1:2967L21 siRNA (2949C) TT	CAUCAGAGGCCCUCCUUGCTT	451
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31187	FLT1:3930L21 siRNA (3912C) TT	GGUUUUGAUUCUUUCCAGGTT	452
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31188	FLT1:349U21 siRNA stab04	B cuGAGuuuAAAAGGcAcccTT B	453
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31189	FLT1:2949U21 siRNA stab04	B GcAAGGAGGGccucuGAuGTT B	454
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31190	FLT1:3912U21 siRNA stab04	B ccuGGAAAGAAucAAAAccTT B	455
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31191	FLT1:367L21 siRNA (349C) stab05	GGGuGccuuuuAAAcucAGTsT	456
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31192	FLT1:2967L21 siRNA (2949C) stab05	cAucAGAGGcccuccuuGcTsT	457
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31193	FLT1:3930L21 siRNA (3912C) stab05	GGuuuuGAuucuuuccAGGTsT	458
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31194	FLT1:349U21 siRNA stab07	B cu*GAGuuuAAAAGGcAcccTT* B	459
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31195	FLT1:2949U21 siRNA stab07	B *GcAAGGAGGGccucuGAuGTT* B	460
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31196	FLT1:3912U21 siRNA stab07	B ccu*GGAAAGAAucAAAAccTT* B	461

FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31197	FLT1:367L21 siRNA (349C) stab08	GGGuGccuuuuAAAcucAGTsT	462
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31198	FLT1:2967L21 siRNA (2949C) stab08	cAucAGAGGcccuccuuGcTsT	463
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31199	FLT1:3930L21 siRNA (3912C) stab08	GGuuuuGAuucuuuccAGGTsT	464
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31200	FLT1:349U21 siRNA inv TT	CCCACGGAAAAUUUGAGUCTT	465
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31201	FLT1:2949U21 siRNA inv TT	GUAGUCUCCGGGAGGAACGTT	466
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31202	FLT1:3912U21 siRNA inv TT	CCAAAACUAAGAAAGGUCCTT	467
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31203	FLT1:367L21 siRNA (349C) inv TT	GACUCAAAUUUUCCGUGGGTT	468
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31204	FLT1:2967L21 siRNA (2949C) inv TT	CGUUCCUCCCGGAGACUACTT	469
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31205	FLT1:3930L21 siRNA (3912C) inv TT	GGACCUUUCUUAGUUUUGGTT	470
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31206	FLT1:349U21 siRNA stab04 inv	B cccAcGGAAAAuuuGAGucTT B	471
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31207	FLT1:2949U21 siRNA stab04 inv	B GuAGucuccGGGAGGAAcGTT B	472
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31208	FLT1:3912U21 siRNA stab04 inv	B ccAAAAcuAAGAAAGGuccTT B	473
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31209	FLT1:367L21 siRNA (349C) stab05 inv	GAcucAAAuuuuccGuGGGTsT	474
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31210	FLT1:2967L21 siRNA (2949C) stab05 inv	cGuuccucccGGAGAcuAcTsT	475
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31211	FLT1:3930L21 siRNA (3912C) stab05 inv	GGAccuuucuuAGuuuuGGTsT	476
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31212	FLT1:349U21 siRNA stab07 inv	B cccAc*GGAAAA*uuu*GA*GucTT B	477
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31213	FLT1:2949U21 siRNA stab07 inv	B *GuAG*ucucc*GGGAGGAAcG*TT B	478
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31214	FLT1:3912U21 siRNA stab07 inv	B cc*AAAAcuAAGAAAGG*uccTT B	479
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31215	FLT1:367L21 siRNA (349C) stab08 inv	GAcucAAAuuuuccGuGGGTsT	480
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31216	FLT1:2967L21 siRNA (2949C) stab08 inv	cGuuccucccGGAGAcuAcTsT	481
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31217	FLT1:3930L21 siRNA (3912C) stab08 inv	GGAccuuucuuAGuuuuGGTsT	482

WO 03/074654 PCT/US03/05028

FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31270	FLT1:349U21 siRNA stab09	B CUGAGUUUAAAAGGCACCCTT B	483
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31271	FLT1:2949U21 siRNA stab09	B GCAAGGAGGGCCUCUGAUGTT B	484
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31272	FLT1:3912U21 siRNA stab09	B CCUGGAAAGAAUCAAAACCTT B	485
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31273	FLT1:367L21 siRNA (349C) stab10	GGGUGCCUUUUAAACUCAGTsT	486
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31274	FLT1:2967L21 siRNA (2949C) stab10	CAUCAGAGGCCCUCCUUGCTsT	487
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31275	FLT1:3930L21 siRNA (3912C) stab10	GGUUUUGAUUCUUUCCAGGTsT	488
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	sense	31276	FLT1:349U21 siRNA stab09 inv	B CCCACGGAAAAUUUGAGUCTT B	489
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	sense	31277	FLT1:2949U21 siRNA stab09 inv	B GUAGUCUCCGGGAGGAACGTT B	490
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	sense	31278	FLT1:3912U21 siRNA stab09 inv	B CCAAAACUAAGAAAGGUCCTT B	491
FLT1	347	AACUGAGUUUAAAAGGCACCCAG	56	antisense	31279	FLT1:367L21 siRNA (349C) stab10 inv	GACUCAAAUUUUCCGUGGGTsT	492
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31280	FLT1:2967L21 siRNA (2949C) stab10 inv	CGUUCCUCCCGGAGACUACTsT	493
FLT1	3910	AGCCUGGAAAGAAUCAAAACCUU	58	antisense	31281	FLT1:3930L21 siRNA (3912C) stab10 inv	GGACCUUUCUUAGUUUUGGTsT	494
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	31424	FLT1:2358L21 siRNA (2340C) stab11 3'-BrdU	uuGuuGuAuuuuGuGGuuGXsX	495
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31425	FLT1:2967L21 siRNA (2949C) stab11 3'-BrdU	cAucAGAGGcccuccuuGcXsX	496
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	31442	FLT1:2358L21 siRNA (2340C) stab11 3'-BrdU	uuGuuGuAuuuuGuGGuuGXsT	497
FLT1	2947	AAGCAAGGAGGGCCUCUGAUGGU	59	antisense	31443	FLT1:2967L21 siRNA (2949C) stab11 3'-BrdU	cAucAGAGGcccuccuuGcXsT	498
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	31449	FLT1:2340U21 siRNA stab09	B CAACCACAAAAUACAACAATT B	499
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	sense	31450	FLT1:2340U21 siRNA inv stab09	B AACAACAUAAAACACCAACTT B	500
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	31451	FLT1:2358L21 siRNA (2340C) stab10	UUGUUGUAUUUUGUGGUUGTsT	501
FLT1	2338	AACAACCACAAAAUACAACAAGA	57	antisense	31452	FLT1:2358L21 siRNA (2340C) inv stab10	GUUGGUGUUUUAUGUUGUUTsT	502
FOS	17	AGCAACUGAGAAGCCAAGACUGA	64	sense	30769	FOS:19U21 siRNA stab04	B cAAcuGAGAAGccAAGAcuTT B	503
FOS	1026	GACAUGGACCUAUCUGGGUCCUU	65	sense	30770	FOS:1028U21 siRNA	B cAuGGAccuAucuGGGuccTT B	504

WO 03/074654 PCT/US03/05028

						stab04		
FOS	1403	UAGGGAGGACCUUAUCUGUGCGU	66	sense	30771	FOS:1405U21 siRNA stab04	B GGGAGGAccuuAucuGuGcTT B	505
FOS	1460	AAGCAUCCAUGUGUGGACUCAAG	67	sense	30772	FOS:1462U21 siRNA stab04	B GcAuccAuGuGuGGAcucATT B	506
FOS	17	AGCAACUGAGAAGCCAAGACUGA	64	antisense	30773	FOS:37L21 siRNA (19C) stab05	AGucuuGGcuucucAGuuGTsT	507
FOS	1026	GACAUGGACCUAUCUGGGUCCUU	65	antisense	30774	FOS:1046L21 siRNA (1028C) stab05	GGAcccAGAuAGGuccAuGTsT	508
FOS	1403	UAGGGAGGACCUUAUCUGUGCGU	66	antisense	30775	FOS:1423L21 siRNA (1405C) stab05	GcAcAGAuAAGGuccucccTsT	509
FOS	1460	AAGCAUCCAUGUGUGGACUCAAG	67	antisense	30776	FOS:1480L21 siRNA (1462C) stab05	uGAGuccAcAcAuGGAuGcTsT	510
FOS	17	AGCAACUGAGAAGCCAAGACUGA	64	sense	31049	FOS:19U21 siRNA	CAACUGAGAAGCCAAGACUTT	511
FOS	1026	GACAUGGACCUAUCUGGGUCCUU	65	sense	31050	FOS:1028U21 siRNA	CAUGGACCUAUCUGGGUCCTT	512
FOS	1403	UAGGGAGGACCUUAUCUGUGCGU	66	sense	31051	FOS:1405U21 siRNA	GGGAGGACCUUAUCUGUGCTT	513
FOS	1460	AAGCAUCCAUGUGUGGACUCAAG	67	sense	31052	FOS:1462U21 siRNA	GCAUCCAUGUGUGGACUCATT	514
FOS	17	AGCAACUGAGAAGCCAAGACUGA	64	antisense	31125	FOS:37L21 siRNA (19C)	AGUCUUGGCUUCUCAGUUGTT	515
FOS	1026	GACAUGGACCUAUCUGGGUCCUU	65	antisense	31126	FOS:1046L21 siRNA (1028C)	GGACCCAGAUAGGUCCAUGTT	516
FOS	1403	UAGGGAGGACCUUAUCUGUGCGU	66	antisense	31127	FOS:1423L21 siRNA (1405C)	GCACAGAUAAGGUCCUCCCTT	517
FOS	1460	AAGCAUCCAUGUGUGGACUCAAG	67	antisense	31128	FOS:1480L21 siRNA (1462C)	UGAGUCCACACAUGGAUGCTT	518
GAB2	2681	UGAAGAGGGAAAGCUGACAUCUG	68	sense	31541	GAB2:2681U21 siRNA	AAGAGGGAAAGCUGACAUCTT	519
GAB2	4316	GAGGAAGAAGGAAGGAGAGGCUU	69	sense	31542	GAB2:4316U21 siRNA	GGAAGAAGGAAGGAGAGGCTT	520
GAB2	5006	GAGAGGACUGAGCCUACGGAAAG	70	sense	31543	GAB2:5006U21 siRNA	GAGGACUGAGCCUACGGAATT	521
GAB2	5958	UUUGCUGUGGUGACACAUGGUAC	71	sense	31544	GAB2:5958U21 siRNA	UGCUGUGGUGACACAUGGUTT	522
GAB2	2699	UGAAGAGGGAAAGCUGACAUCUG	68	antisense	31545	GAB2:2699L21 siRNA (2681C)	GAUGUCAGCUUUCCCUCUUTT	523
GAB2	4334	GAGGAAGAAGGAAGGAGAGGCUU	69	antisense	31546	GAB2:4334L21 siRNA (4316C)	GCCUCUCCUUCCUUCUUCCTT	524
GAB2	5024	GAGAGGACUGAGCCUACGGAAAG	70	antisense	31547	GAB2:5024L21 siRNA (5006C)	UUCCGUAGGCUCAGUCCUCTT	525
GAB2	5976	UUUGCUGUGGUGACACAUGGUAC	71	antisense	31548	GAB2:5976L21 siRNA (5958C)	ACCAUGUGUCACCACAGCATT	526
Her2		CCGCAGUGAGCACCAUGGA	72	antisense	25245	RPI 17763 Her2Neu AS as siRNA Str 2 (antisense)	B UCCAUGGUGCUCACUGCGGCU B	527
Her2		AGCCGCAGUGAGCACCAUG	73	sense	25246	RPI 17763 Her2Neu AS as siRNA Str 1 (sense)	B AGCCGCAGUGAGCACCAUGGA B	528
Her2		CCGCAGUGAGCACCAUGGA	72	sense	25247	RPI 17763 Her2Neu AS	B AGGUACCACGAGUGACGCCGA B	529

						as siRNA Str 1 (sense) Inverted control		
Her2		CAUGGUGCUCACUGCGGCU	74	sense	25248	RPI 17763 Her2Neu AS as siRNA Str 1 (sense) Inverted control compliment	B UCGGCGUCACUCGUGGUACCU B	530
Her2		CCGCAGUGAGCACCAUGGA	72	antisense	25822	RPI 17763 Her2Neu AS as siRNA Str 2 (antisense)+2U overhang	UCCAUGGUGCUCACUGCGGCUUU	531
Her2		AGCCGCAGUGAGCACCAUG	73	sense	25823	RPI 17763 Her2Neu AS as siRNA Str 1 (sense)+2U overhang	AGCCGCAGUGAGCACCAUGGAUU	532
Her2		CCGCAGUGAGCACCAUGGA	72	antisense	25842	RPI 17763 Her2Neu AS as siRNA Str 2 (antisense)+2U overhang	B UCCAUGGUGCUCACUGCGGCUUU B	533
Her2		AGCCGCAGUGAGCACCAUG	73	sense	25843	RPI 17763 Her2Neu AS as siRNA Str 1 (sense)+2U overhang	B AGCCGCAGUGAGCACCAUGGAUU B	534
Her2		UGGGGUCGUCAAAGACGUU	75	sense	28262	Her2.1.sense Str1	UGGGGUCGUCAAAGACGUUTT	535
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	28263	Her2.1.antisense Str2	AACGUCUUUGACGACCCCATT	536
Her2		UGGGGUCGUCAAAGACGUU	75	sense	28264	Her2.1.sense Str1 inverted	UUGCAGAAACUGCUGGGGUTT	537
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	28265	Her2.1.antisense Str2 inverted	ACCCCAGCAGUUUCUGCAATT	538
Her2		GGUGCUUGGAUCUGGCGCU	76	sense	28266	Her2.2.sense Str1	GGUGCUUGGAUCUGGCGCUTT	539
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	28267	Her2.2.antisense Str2	AGCGCCAGAUCCAAGCACCTT	540
Her2		GGUGCUUGGAUCUGGCGCU	76	sense	28268	Her2.2.sense Str1 inverted	UCGCGGUCUAGGUUCGUGGTT	541
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	28269	Her2.2.antisense Str2 inverted	CCACGAACCUAGACCGCGATT	542
Her2		GAUCUUUGGGAGCCUGGCA	77	sense	28270	Her2.3.sense Str1	GAUCUUUGGGAGCCUGGCATT	543
Her2		GAUCUUUGGGAGCCUGGCA	77	antisense	28271	Her2.3.antisense Str2	UGCCAGGCUCCCAAAGAUCTT	544
Her2		GAUCUUUGGGAGCCUGGCA	77	sense	28272	Her2.3.sense Str1 inverted	ACGGUCCGAGGGUUUCUAGTT	545
Her2		GAUCUUUGGGAGCCUGGCA	77	antisense	28273	Her2.3.antisense Str2 inverted	CUAGAAACCCUCGGACCGUTT	546
Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	29989	Her2.2.sense Str1 (site 2344)	GsGsusGscuuGGAucuGGcGscsusTsT	547
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	29990	Her2.2.antisense Str2	AsGsCsGsCsCAGAUCCAAGCACCTsT	548
Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	29991	Her2.2.sense Str1 (site 2344)	GsGsUsGsCsUUGGAUCUGGCGCUTsT	549

Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	29992	Her2.2.sense Str1 (site 2344)	GsGsusGscuuGGAucuGGcGcuTTB	550
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	29993	Her2.2.antisense Str2	AsGsCsGsCsCsAsGsAsUsCsCsAsAsGsCsAsCsCsTsT	551
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	29994	Her2.2.antisense Str2	AsGsCsGsCsCsAsGsAsUsCCAAGCACCTsT	552
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	29995	Her2.2.antisense Str2	AsGsCsGsCsCsAsGsAsUsCsCsAsAsGCACCTsT	553
Her2		GGUGCUUGGAUCUGGCGCU	76	sense	29996	Her2.2.sense Str1 inverted	uscsGscsGGucuAGGuucGusGsGsTsT	554
Her2		GGUGCUUGGAUCUGGCGCU	76	sense	29997	Her2.2.sense Str1 inverted	UsCsGsCsGsGUCUAGGUUCGUGGTsT	555
Her2		GGUGCUUGGAUCUGGCGCU	76	sense	29998	Her2.2.sense Str1 inverted	uscsGscsGGucuAGGuucGuGGTTB	556
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	29999	Her2.2.antisense Str2 inverted	CsCsAsCsGsAACCUAGACCGCGATsT	557
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30000	Her2.2.antisense Str2 inverted	CsCsAsCsGsAsAsCsCsUsAsGsAsCsCsGsCsGsAsTsT	558
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30001	Her2.2.antisense Str2 inverted	CsCsAsCsGsAsAsCsCsUsAGACCGCGATsT	559
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30002	Her2.2.antisense Str2 inverted	CsCsAsCsGsAsAsCsCsUsAsGsAsCsCGCGATsT	560
Her2	3704	UGGGGUCGUCAAAGACGUU	75	sense	30438	Her2 sense (site 3706) stab4	B uGGGGucGucAAAGAcGuuTT B	561
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30439	Her2 antisense (site 3706) stab5	AAcGucuuuGAcGAccccATsT	562
Her2	3704	UGGGGUCGUCAAAGACGUU	75	sense	30440	Her2 sense inverted (site 3706) stab4	B uuGcAGAAAcuGcuGGGGuTT B	563
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30441	Her2 antisense inverted (site 3706) stab5	AccccAGcAGuuucuGcAATsT	564
Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	30442	Her2 sense (site 2344) stab4	B GGuGcuuGGAucuGGcGcuTT B	565
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30443	Her2 antisense (site 2344) stab5	AGcGccAGAuccAAGcAccTsT	566
Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	30444	Her2 sense inverted (site 2344) stab4	B ucGcGGucuAGGuucGuGGTT B	567
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30445	Her2 antisense inverted (site 2344) stab5	ccAcGAAccuAGAccGcGATsT	568
Her2	3704	UGGGGUCGUCAAAGACGUU	75	sense	30446	Her2 sense Str1 site 3706 stab6	B uGGGGucGucAAAGAcGuuTT B	569
Her2	3704	UGGGGUCGUCAAAGACGUU	75	sense	30447	Her2 sense inverted (site 3706) stab6	B uuGcAGAAAcuGcuGGGGuTT B	570

Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	30448	Her2 sense (site 2344) stab6	B GGuGcuuGGAucuGGcGcuTT B	571
Her2	2342	GGUGCUUGGAUCUGGCGCU	76	sense	30449	Her2 sense inverted (site 2344) stab6	B ucGcGGucuAGGuucGuGGTT B	572
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	sense	30645	HER2:2346U21 siRNA stab07	B *GGuGcuuGGAucuGGcGcu*TT B	573
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30646	HER2:3726L21 siRNA (3708C) stab07	B *AAcGucuuuGAcGAccccA*TT B	574
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30647	HER2:2364L21 siRNA (2346C) stab08	AGcGccAGAuccAAGcAccTsT	575
Her2	3706	UGGGGUCGUCAAAGACGUU	75	sense	30648	HER2:3708U21 siRNA stab08	uGGGGucGucAAAGAcGuuTsT	576
Her2	1882	GAAUGGCUCAGUGACCUGU	78	sense	30697	HER2:1884U21 siRNA stab04	B GAAuGGcucAGuGAccuGuTT B	577
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	sense	30698	HER2:2346U21 siRNA stab04	B GGuGcuuGGAucuGGcGcuTT B	565
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30699	HER2:3726L21 siRNA (3708C) stab04	B AAcGucuuuGAcGAccccATT B	578
Her2	3877	CACCUUCAAAGGGACACCU	79	sense	30700	HER2:3879U21 siRNA stab04	B cAccuucAAAGGGAcAccuTT B	579
Her2	1882	GAAUGGCUCAGUGACCUGU	78	antisense	30701	HER2:1902L21 siRNA (1884C) stab05	AcAGGucAcuGAGccAuucTsT	580
Her2	2344	GGUGCUUGGAUCUGGCGCU	76	antisense	30702	HER2:2364L21 siRNA (2346C) stab05	AGcGccAGAuccAAGcAccTsT	566
Her2	3706	UGGGGUCGUCAAAGACGUU	75	sense	30703	HER2:3708U21 siRNA stab05	uGGGGucGucAAAGAcGuuTsT	581
Her2	3877	CACCUUCAAAGGGACACCU	79	antisense	30704	HER2:3897L21 siRNA (3879C) stab05	AGGuGucccuuuGAAGGuGTsT	582
Her2	3706	UGGGGUCGUCAAAGACGUU	75	sense	30951	HER2:3708U21 siRNA stab07	B u*GGGGucGucAAAGAcGuu*TT B	583
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30952	HER2:3726L21 siRNA (3708C) stab08	AAcGucuuuGAcGAccccATsT	584
Her2	3706	UGGGGUCGUCAAAGACGUU	75	sense	30953	HER2:3708U21 siRNA stab04	B uGGGGucGucAAAGAcGuuTT B	561
Her2	3706	UGGGGUCGUCAAAGACGUU	75	antisense	30954	HER2:3726L21 siRNA (3708C) stab05	AAcGucuuuGAcGAccccATsT	562
HRAS	77	GAACCAUUUUGUGGACGAAUACG	80	sense	31525	HRAS:77U21 siRNA	ACCAUUUUGUGGACGAAUATT	585
HRAS	154	GCCUGUUGGACAUCCUGGAUACC	81	sense	31526	HRAS:154U21 siRNA	CUGUUGGACAUCCUGGAUATT	586
HRAS	459	GAGGAUGCCUUCUACACGUUGGU	82	sense	31527	HRAS:459U21 siRNA	GGAUGCCUUCUACACGUUGTT	587
HRAS	513	CUGAACCCUCCUGAUGAGAGUGG	83	sense	31528	HRAS:513U21 siRNA	GAACCCUCCUGAUGAGAGUTT	588
HRAS	95	GAACCAUUUUGUGGACGAAUACG	80	antisense	31529	HRAS:95L21 siRNA (77C)	UAUUCGUCCACAAAAUGGUTT	589

HRAS	172	GCCUGUUGGACAUCCUGGAUACC	81	antisense	31530	HRAS:172L21 siRNA (154C)	UAUCCAGGAUGUCCAACAGTT	590
HRAS	477	GAGGAUGCCUUCUACACGUUGGU	82	antisense	31531	HRAS:477L21 siRNA (459C)	CAACGUGUAGAAGGCAUCCTT	591
HRAS	531	CUGAACCCUCCUGAUGAGAGUGG	83	antisense	31532	HRAS:531L21 siRNA (513C)	ACUCUCAUCAGGAGGGUUCTT	592
hTR	31	UCAGCUUGGCCAAUCCGUGCGGU	84	sense	29950	hTR:33U21 siRNA	AGCUUGGCCAAUCCGUGCGGU	593
hTR	99	GGUUGCGGAGGGUGGGCCUGGGA	85	sense	29951	hTR:101U21 siRNA	UUGCGGAGGGUGGGCCUGGGA	594
hTR	233	GCCUGCCGCCUUCCACCGUUCAU	86	sense	29952	hTR:235U21 siRNA	CUGCCGCCUUCCACCGUUCAU	595
hTR	380	GCACCCACUGCCACCGCGAAGAG	87	sense	29953	hTR:382U21 siRNA	ACCCACUGCCACCGCGAAGAG	596
hTR	492	GCGCGGCGCGAUUCCCUGAGCUG	88	sense	29954	hTR:494U21 siRNA	GCGGCGCGAUUCCCUGAGCUG	597
hTR	31	UCAGCUUGGCCAAUCCGUGCGGU	84	antisense	29955	hTR:53L21 siRNA (33C)	CGCACGGAUUGGCCAAGCUGA	598
hTR	99	GGUUGCGGAGGGUGGGCCUGGGA	85	antisense	29956	hTR:121L21 siRNA (101C)	CCAGGCCCACCCUCCGCAACC	599
hTR	233	GCCUGCCGCCUUCCACCGUUCAU	86	antisense	29957	hTR:255L21 siRNA (235C)	GAACGGUGGAAGGCGGCAGGC	600
hTR	380	GCACCCACUGCCACCGCGAAGAG	87	antisense	29958	hTR:402L21 siRNA (382C)	CUUCGCGGUGGCAGUGGGUGC	601
hTR	492	GCGCGGCGCGAUUCCCUGAGCUG	88	antisense	29959	hTR:514L21 siRNA (494C)	GCUCAGGGAAUCGCGCCGCGC	602
hTR	62	GCUCCCUUUAUAAGCCGACUCGC	89	sense	30913	hTR:64U21 siRNA stab04	B ucccuuuAuAAGccGAcucTT B	603
hTR	241	CCUUCCACCGUUCAUUCUAGAGC	90	sense	30914	hTR:243U21 siRNA stab04	B uuccAccGuucAuucuAGATT B	604
hTR	243	UUCCACCGUUCAUUCUAGAGCAA	91	sense	30915	hTR:245U21 siRNA stab04	B ccAccGuucAuucuAGAGcTT B	605
hTR	395	GCGAAGAGUUGGGCUCUGUCAGC	92	sense	30916	hTR:397U21 siRNA stab04	B GAAGAGuuGGGcucuGucATT B	606
hTR	62	GCUCCCUUUAUAAGCCGACUCGC	89	antisense	30917	hTR:82L21 siRNA (64C) stab05	GAGucGGcuuAuAAAGGGATsT	607
hTR	241	CCUUCCACCGUUCAUUCUAGAGC	90	antisense	30918	hTR:261L21 siRNA (243C) stab05	ucuAGAAuGAAcGGuGGAATsT	608
hTR	243	UUCCACCGUUCAUUCUAGAGCAA	91	antisense	30919	hTR:263L21 siRNA (245C) stab05	GcucuAGAAuGAAcGGuGGTsT	609
hTR	395	GCGAAGAGUUGGGCUCUGUCAGC	92	antisense	30920	hTR:415L21 siRNA (397C) stab05	uGAcAGAGcccAAcucuucTsT	610
IKKg	166	UGGAAGAGCCAACUGUGUGAGAU	93	sense	30801	IKKg:166U21 siRNA stab04	B GAAGAGccAAcuGuGuGAGTT B	611
IKKg	407	AGAGGGAGGAGAAGGAGUUCCUC	94	sense	30802	IKKg:407U21 siRNA stab04	B AGGGAGGAGAAGGAGuuccTT B	612
IKKg	1162	AGGGAGUACAGCAAACUGAAGGC	95	sense	30803	IKKg:1162U21 siRNA stab04	B GGAGuAcAGcAAAcuGAAGTT B	613

WO 03/074654 PCT/US03/05028

IKKg	1390	GUCAUGGAGUGCAUUGAGUAGGG	96	sense	30804	IKKg:1390U21 siRNA stab04	B cAuGGAGuGcAuuGAGuAGTT B	614
IKKg	184	UGGAAGAGCCAACUGUGUGAGAU	93	antisense	30805	IKKg:184L21 siRNA (166C) stab05	cucAcAcAGuuGGcucuucTsT	615
IKKg	425	AGAGGGAGGAGAAGGAGUUCCUC	94	antisense	30806	IKKg:425L21 siRNA (407C) stab05	GGAAcuccuucuccucccuTsT	616
IKKg	1180	AGGGAGUACAGCAAACUGAAGGC	95	antisense	30807	IKKg:1180L21 siRNA (1162C) stab05	cuucAGuuuGcuGuAcuccTsT	617
IKKg	1408	GUCAUGGAGUGCAUUGAGUAGGG	96	antisense	30808	IKKg:1408L21 siRNA (1390C) stab05	cuAcucAAuGcAcuccAuGTsT	618
IL2	28	UAACCUCAACUCCUGCCACAAUG	97	sense	30809	IL2:30U21 siRNA stab04	B AccucAAcuccuGccAcAATT B	619
IL2	61	AACUCCUGUCUUGCAUUGCACUA	98	sense	30810	IL2:63U21 siRNA stab04	B cuccuGucuuGcAuuGcAcTT B	620
IL2	86	UCUUGCACUUGUCACAAACAGUG	99	sense	30811	IL2:88U21 siRNA stab04	B uuGcAcuuGucAcAAAcAGTT B	621
IL2	143	AACACAGCUACAACUGGAGCAUU	100	sense	30812	IL2:145U21 siRNA stab04	B cAcAGcuAcAAcuGGAGcATT B	622
IL2	28	UAACCUCAACUCCUGCCACAAUG	97	antisense	30813	IL2:48L21 siRNA (30C) stab05	uuGuGGcAGGAGuuGAGGuTsT	623
IL2	61	AACUCCUGUCUUGCAUUGCACUA	98	antisense	30814	IL2:81L21 siRNA (63C) stab05	GuGcAAuGcAAGAcAGGAGTsT	624
IL2	86	UCUUGCACUUGUCACAAACAGUG	99	antisense	30815	IL2:106L21 siRNA (88C) stab05	cuGuuuGuGAcAAGuGcAATsT	625
IL2	143	AACACAGCUACAACUGGAGCAUU	100	antisense	30816	IL2:163L21 siRNA (145C) stab05	uGcuccAGuuGuAGcuGuGTsT	626
IL2	28	UAACCUCAACUCCUGCCACAAUG	97	sense	31400	IL2:30U21 siRNA	ACCUCAACUCCUGCCACAATT	627
IL2	61	AACUCCUGUCUUGCAUUGCACUA	98	sense	31401	IL2:63U21 siRNA	CUCCUGUCUUGCAUUGCACTT	628
IL2	86	UCUUGCACUUGUCACAAACAGUG	99	sense	31402	IL2:88U21 siRNA	UUGCACUUGUCACAAACAGTT	629
IL2	143	AACACAGCUACAACUGGAGCAUU	100	sense	31403	IL2:145U21 siRNA	CACAGCUACAACUGGAGCATT	630
IL2	28	UAACCUCAACUCCUGCCACAAUG	97	antisense	31404	IL2:48L21 siRNA (30C)	UUGUGGCAGGAGUUGAGGUTT	631
IL2	61	AACUCCUGUCUUGCAUUGCACUA	98	antisense	31405	IL2:81L21 siRNA (63C)	GUGCAAUGCAAGACAGGAGTT	632
IL2	86	UCUUGCACUUGUCACAAACAGUG	99	antisense	31406	IL2:106L21 siRNA (88C)	CUGUUUGUGACAAGUGCAATT	633
IL2	143	AACACAGCUACAACUGGAGCAUU	100	antisense	31407	IL2:163L21 siRNA (145C)	UGCUCCAGUUGUAGCUGUGTT	634
KDR	3074	UGUCCACUUACCUGAGGAGCAAG	101	sense	30785	KDR:3076U21 siRNA stab04	B uccAcuuAccuGAGGAGcATT B	635
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	sense	30786	KDR:3854U21 siRNA stab04	B uGAGcAuGGAAGAGGAuucTT B	636
KDR	4087	AUGGUUCUUGCCUCAGAAGAGCU	103	sense	30787	KDR:4089U21 siRNA stab04	B GGuucuuGccucAGAAGAGTT B	637
KDR	4189	UCUGAAGGCUCAAACCAGACAAG	104	sense	30788	KDR:4191U21 siRNA stab04	B uGAAGGcucAAAccAGAcATT B	638
KDR	3074	UGUCCACUUACCUGAGGAGCAAG	101	antisense	30789	KDR:3094L21 siRNA (3076C) stab05	uGcuccucAGGuAAGuGGATsT	639
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	antisense	30790	KDR:3872L21 siRNA	GAAuccucuuccAuGcucATsT	640

WO 03/074654 PCT/US03/05028

						(3854C) stab05		
KDR	4087	AUGGUUCUUGCCUCAGAAGAGCU	103	antisense	30791	KDR:4107L21 siRNA (4089C) stab05	cucuucuGAGGcAAGAAccTsT	641
KDR	4189	UCUGAAGGCUCAAACCAGACAAG	104	antisense	30792	KDR:4209L21 siRNA (4191C) stab05	uGucuGGuuuGAGccuucATsT	642
KDR	3074	UGUCCACUUACCUGAGGAGCAAG	101	sense	31426	KDR:3076U21 siRNA	UCCACUUACCUGAGGAGCATT	643
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	sense	31427	KDR:3854U21 siRNA	UGAGCAUGGAAGAGGAUUCTT	644
KDR	4087	AUGGUUCUUGCCUCAGAAGAGCU	103	sense	31428	KDR:4089U21 siRNA	GGUUCUUGCCUCAGAAGAGTT	645
KDR	4189	UCUGAAGGCUCAAACCAGACAAG	104	sense	31429	KDR:4191U21 siRNA	UGAAGGCUCAAACCAGACATT	646
KDR	3074	UGUCCACUUACCUGAGGAGCAAG	101	antisense	31430	KDR:3094L21 siRNA (3076C)	UGCUCCUCAGGUAAGUGGATT	647
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	antisense	31431	KDR:3872L21 siRNA (3854C)	GAAUCCUCUUCCAUGCUCATT	648
KDR	4087	AUGGUUCUUGCCUCAGAAGAGCU	103	antisense	31432	KDR:4107L21 siRNA (4089C)	CUCUUCUGAGGCAAGAACCTT	649
KDR	4189	UCUGAAGGCUCAAACCAGACAAG	104	antisense	31433	KDR:4209L21 siRNA (4191C)	UGUCUGGUUUGAGCCUUCATT	650
KDR	3302	UGACCUUGGAGCAUCUCAUCUGU	105	sense	31434	KDR:3304U21 siRNA	ACCUUGGAGCAUCUCAUCUTT	651
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	sense	31435	KDR:3854U21 siRNA	UGAGCAUGGAAGAGGAUUCTT	644
KDR	3892	UCACCUGUUUCCUGUAUGGAGGA	106	sense	31436	KDR:3894U21 siRNA	ACCUGUUUCCUGUAUGGAGTT	652
KDR	3946	GACAACACAGCAGGAAUCAGUCA	107	sense	31437	KDR:3948U21 siRNA	CAACACAGCAGGAAUCAGUTT	653
KDR	3302	UGACCUUGGAGCAUCUCAUCUGU	105	antisense	31438	KDR:3322L21 siRNA (3304C)	AGAUGAGAUGCUCCAAGGUTT	654
KDR	3852	UUUGAGCAUGGAAGAGGAUUCUG	102	antisense	31439	KDR:3872L21 siRNA (3854C)	GAAUCCUCUUCCAUGCUCATT	648
KDR	3892	UCACCUGUUUCCUGUAUGGAGGA	106	antisense	31440	KDR:3912L21 siRNA (3894C)	CUCCAUACAGGAAACAGGUTT	655
KDR	3946	GACAACACAGCAGGAAUCAGUCA	107	antisense	31441	KDR:3966L21 siRNA (3948C)	ACUGAUUCCUGCUGUGUUGTT	656
KRAS2	625	ACAAGACAGGGUGUUGAUGAUGC	108	sense	31533	KRAS2:625U21 siRNA	AAGACAGGGUGUUGAUGAUTT	657
KRAS2	625	ACAAGACAGGGUGUUGAUGAUGC	108	sense	31533	KRAS2:625U21 siRNA	AAGACAGGGUGUUGAUGAUTT	657
KRAS2	920	UUUCCUCGAAGUGCCAGUAUUCC	109	sense	31534	KRAS2:920U21 siRNA	UCCUCGAAGUGCCAGUAUUTT	658
KRAS2	920	UUUCCUCGAAGUGCCAGUAUUCC	109	sense	31534	KRAS2:920U21 siRNA	UCCUCGAAGUGCCAGUAUUTT	658
KRAS2	999	AUUUCUGUCUUGGGGUUUUUGGU	110	sense	31535	KRAS2:999U21 siRNA	UUCUGUCUUGGGGUUUUUGTT	659
KRAS2	999	AUUUCUGUCUUGGGGUUUUUGGU	110	sense	31535	KRAS2:999U21 siRNA	UUCUGUCUUGGGGUUUUUGTT	659
KRAS2	1013	GUUUUUGGUGCAUGCAGUUGAUU	111	sense	31536	KRAS2:1013U21 siRNA	UUUUGGUGCAUGCAGUUGATT	660
KRAS2	1013	GUUUUUGGUGCAUGCAGUUGAUU	111	sense	31536	KRAS2:1013U21 siRNA	UUUUGGUGCAUGCAGUUGATT	660
KRAS2	643	ACAAGACAGGGUGUUGAUGAUGC	108	antisense	31537	KRAS2:643L21 siRNA (625C)	AUCAUCAACACCCUGUCUUTT	661
KRAS2	643	ACAAGACAGGGUGUUGAUGAUGC	108	antisense	31537	KRAS2:643L21 siRNA	AUCAUCAACACCCUGUCUUTT	661

WO 03/074654 PCT/US03/05028

						(625C)		
KRAS2	938	UUUCCUCGAAGUGCCAGUAUUCC	109	antisense	31538	KRAS2:938L21 siRNA (920C)	AAUACUGGCACUUCGAGGATT	662
KRAS2	938	UUUCCUCGAAGUGCCAGUAUUCC	109	antisense	31538	KRAS2:938L21 siRNA (920C)	AAUACUGGCACUUCGAGGATT	662
KRAS2	1017	AUUUCUGUCUUGGGGUUUUUGGU	110	antisense	31539	KRAS2:1017L21 siRNA (999C)	CAAAAACCCCAAGACAGAATT	663
KRAS2	1017	AUUUCUGUCUUGGGGUUUUUGGU	110	antisense	31539	KRAS2:1017L21 siRNA (999C)	CAAAAACCCCAAGACAGAATT	663
KRAS2	1031	GUUUUUGGUGCAUGCAGUUGAUU	111	antisense	31540	KRAS2:1031L21 siRNA (1013C)	UCAACUGCAUGCACCAAAATT	664
KRAS2	1031	GUUUUUGGUGCAUGCAGUUGAUU	111	antisense	31540	KRAS2:1031L21 siRNA (1013C)	UCAACUGCAUGCACCAAAATT	664
MAPK1	424	ACCAGACCUACUGCCAGAGAACC	112	sense	30817	MAPK1:424U21 siRNA stab04	B cAGAccuAcuGccAGAGAATT B	665
MAPK1	778	AUCACACAGGGUUCCUGACAGAA	113	sense	30818	MAPK1:778U21 siRNA stab04	B cAcAcAGGGuuccuGAcAGTT B	666
MAPK1	1718	UUGGCUCUAGUCACUGGCAUCUC	114	sense	30819	MAPK1:1718U21 siRNA stab04	B GGcucuAGucAcuGGcAucTT B	667
MAPK1	2525	ACUGUGGAGUUGACUCGGUGUUC	115	sense	30820	MAPK1:2525U21 siRNA stab04	B uGuGGAGuuGAcucGGuGuTT B	668
MAPK1	442	ACCAGACCUACUGCCAGAGAACC	112	antisense	30821	MAPK1:442L21 siRNA (424C) stab05	uucucuGGcAGuAGGucuGTsT	669
MAPK1	796	AUCACACAGGGUUCCUGACAGAA	113	antisense	30822	MAPK1:796L21 siRNA (778C) stab05	cuGucAGGAAcccuGuGuGTsT	670
MAPK1	1736	UUGGCUCUAGUCACUGGCAUCUC	114	antisense	30823	MAPK1:1736L21 siRNA (1718C) stab05	GAuGccAGuGAcuAGAGccTsT	671
MAPK1	2543	ACUGUGGAGUUGACUCGGUGUUC	115	antisense	30824	MAPK1:2543L21 siRNA (2525C) stab05	AcAccGAGucAAcuccAcATsT	672
MAPK14	1280	GCCUACUUUGCUCAGUACCACGA	116	sense	31586	MAPK14:1280U21 siRNA	CUACUUUGCUCAGUACCACTT	673
MAPK14	1611	UGUCUGUCUUUGUGGGAGGGUAA	117	sense	31587	MAPK14:1611U21 siRNA	UCUGUCUUUGUGGGAGGGUTT	674
MAPK14	2884	AAAAGGGUCUUCUUGGCAGCUUA	118	sense	31588	MAPK14:2884U21 siRNA	AAGGGUCUUCUUGGCAGCUTT	675
MAPK14	3556	GGACUCUAAGCUGGAGCUCUUGG	119	sense	31589	MAPK14:3556U21 siRNA	ACUCUAAGCUGGAGCUCUUTT	676
MAPK14	1298	GCCUACUUUGCUCAGUACCACGA	116	antisense	31590	MAPK14:1298L21 siRNA (1280C)	GUGGUACUGAGCAAAGUAGTT	677
MAPK14	1629	UGUCUGUCUUUGUGGGAGGGUAA	117	antisense	31591	MAPK14:1629L21 siRNA (1611C)	ACCCUCCCACAAAGACAGATT	678
MAPK1	2902	AAAAGGGUCUUCUUGGCAGCUUA	118	antisense	31592	MAPK14:2902L21 siRNA	AGCUGCCAAGAAGACCCUUTT	679

4						(2884C)		
MAPK14	3574	GGACUCUAAGCUGGAGCUCUUGG	119	antisense	31593	MAPK14:3574L21 siRNA (3556C)	AAGAGCUCCAGCUUAGAGUTT	680
MAPK8	733	AACAGCUUGGAACACCAUGUCCU	120	sense	31517	MAPK8:735U21 siRNA	CAGCUUGGAACACCAUGUCTT	681
MAPK8	853	UUUUCCCAGCUGACUCAGAACAC	121	sense	31518	MAPK8:855U21 siRNA	UUCCCAGCUGACUCAGAACTT	682
MAPK8	1224	CAAUGUCAACAGAUCCGACUUUG	122	sense	31519	MAPK8:1226U21 siRNA	AUGUCAACAGAUCCGACUUTT	683
MAPK8	1242	CUUUGGCCUCUGAUACAGACAGC	123	sense	31520	MAPK8:1244U21 siRNA	UUGGCCUCUGAUACAGACATT	684
MAPK8	733	AACAGCUUGGAACACCAUGUCCU	120	antisense	31521	MAPK8:753L21 siRNA (735C)	GACAUGGUGUUCCAAGCUGTT	685
MAPK8	853	UUUUCCCAGCUGACUCAGAACAC	121	antisense	31522	MAPK8:873L21 siRNA (855C)	GUUCUGAGUCAGCUGGGAATT	686
MAPK8	1224	CAAUGUCAACAGAUCCGACUUUG	122	antisense	31523	MAPK8:1244L21 siRNA (1226C)	AAGUCGGAUCUGUUGACAUTT	687
MAPK8	1242	CUUUGGCCUCUGAUACAGACAGC	123	antisense	31524	MAPK8:1262L21 siRNA (1244C)	UGUCUGUAUCAGAGGCCAATT	688
MYB	146	AACAACCACAAAAUACAACAAGA	57	sense	30977	MYB:148U21 siRNA stab04	B GuGAcGAGGAuGAuGAGGATT B	689
MYB	455	AACAACCACAAAAUACAACAAGA	57	sense	30978	MYB:457U21 siRNA stab04	B GGucuGuuAuuGccAAGcATT B	690
MYB	706	AACAACCACAAAAUACAACAAGA	57	sense	30979	MYB:708U21 siRNA stab04	B cuGcAGGAGucuucAAAAGTT B	691
MYB	1051	AACAACCACAAAAUACAACAAGA	57	sense	30980	MYB:1053U21 siRNA stab04	B GuGcuAccAAcAcAGAAccTT B	692
MYB	146	AACAACCACAAAAUACAACAAGA	57	antisense	30981	MYB:166L21 siRNA (148C) stab05	uccucAucAuccucGucAcTsT	693
MYB	455	AACAACCACAAAAUACAACAAGA	57	antisense	30982	MYB:475L21 siRNA (457C) stab05	uGcuuGGcAAuAAcAGAccTsT	694
MYB	706	AACAACCACAAAAUACAACAAGA	57	antisense	30983	MYB:726L21 siRNA (708C) stab05	cuuuuGAAGAcuccuGcAGTsT	695
MYB	1051	AACAACCACAAAAUACAACAAGA	57	antisense	30984	MYB:1071L21 siRNA (1053C) stab05	GGuucuGuGuuGGuAGcAcTsT	696
MYB	146	CAGUGACGAGGAUGAUGAGGACU	124	sense	31025	MYB:148U21 siRNA	GUGACGAGGAUGAUGAGGATT	697
MYB	455	UUGGUCUGUUAUUGCCAAGCACU	125	sense	31026	MYB:457U21 siRNA	GGUCUGUUAUUGCCAAGCATT	698
MYB	706	AUCUGCAGGAGUCUUCAAAAGCC	126	sense	31027	MYB:708U21 siRNA	CUGCAGGAGUCUUCAAAAGTT	699
MYB	1051	AGGUGCUACCAACACAGAACCAC	127	sense	31028	MYB:1053U21 siRNA	GUGCUACCAACACAGAACCTT	700
MYB	146	CAGUGACGAGGAUGAUGAGGACU	124	antisense	31101	MYB:166L21 siRNA (148C)	UCCUCAUCAUCCUCGUCACTT	701
MYB	455	UUGGUCUGUUAUUGCCAAGCACU	125	antisense	31102	MYB:475L21 siRNA (457C)	UGCUUGGCAAUAACAGACCTT	702
MYB	706	AUCUGCAGGAGUCUUCAAAAGCC	126	antisense	31103	MYB:726L21 siRNA (708C)	CUUUUGAAGACUCCUGCAGTT	703

WO 03/074654 PCT/US03/05028

MYB	1051	AGGUGCUACCAACACAGAACCAC	127	antisense	31104	MYB:1071L21 siRNA (1053C)	GGUUCUGUGUUGGUAGCACTT	704
MYC	1524	CAAGAGGGUCAAGUUGGACAGUG	128	sense	30825	MYC:1526U21 siRNA stab04	B AGAGGGucAAGuuGGAcAGTT B	705
MYC	1778	AAGCAGAGGAGCAAAAGCUCAUU	129	sense	30826	MYC:1780U21 siRNA stab04	B GcAGAGGAGcAAAAGcucATT B	706
MYC	1859	UACGGAACUCUUGUGCGUAAGGA	130	sense	30827	MYC:1861U21 siRNA stab04	B cGGAAcucuuGuGcGuAAGTT B	707
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	30828	MYC:1971U21 siRNA stab04	B AAccuuGGcuGAGucuuGATT B	708
MYC	1524	CAAGAGGGUCAAGUUGGACAGUG	128	antisense	30829	MYC:1544L21 siRNA (1526C) stab05	cuGuccAAcuuGAcccucuTsT	709
MYC	1778	AAGCAGAGGAGCAAAAGCUCAUU	129	antisense	30830	MYC:1798L21 siRNA (1780C) stab05	uGAGcuuuuGcuccucuGcTsT	710
MYC	1859	UACGGAACUCUUGUGCGUAAGGA	130	antisense	30831	MYC:1879L21 siRNA (1861C) stab05	cuuAcGcAcAAGAGuuccGTsT	711
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	30832	MYC:1989L21 siRNA (1971C) stab05	ucAAGAcucAGccAAGGuuTsT	712
MYC	1524	CAAGAGGGUCAAGUUGGACAGUG	128	sense	30993	MYC:1526U21 siRNA	AGAGGGUCAAGUUGGACAGTT	713
MYC	1778	AAGCAGAGGAGCAAAAGCUCAUU	129	sense	30994	MYC:1780U21 siRNA	GCAGAGGAGCAAAAGCUCATT	714
MYC	1859	UACGGAACUCUUGUGCGUAAGGA	130	sense	30995	MYC:1861U21 siRNA	CGGAACUCUUGUGCGUAAGTT	715
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	30996	MYC:1971U21 siRNA	AACCUUGGCUGAGUCUUGATT	716
MYC	1524	CAAGAGGGUCAAGUUGGACAGUG	128	antisense	31069	MYC:1544L21 siRNA (1526C)	CUGUCCAACUUGACCCUCUTT	717
MYC	1778	AAGCAGAGGAGCAAAAGCUCAUU	129	antisense	31070	MYC:1798L21 siRNA (1780C)	UGAGCUUUUGCUCCUCUGCTT	718
MYC	1859	UACGGAACUCUUGUGCGUAAGGA	130	antisense	31071	MYC:1879L21 siRNA (1861C)	CUUACGCACAAGAGUUCCGTT	719
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	31072	MYC:1989L21 siRNA (1971C)	UCAAGACUCAGCCAAGGUUTT	720
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	31377	MYC:1971U21 siRNA stab04	B AAccuuGGcuGAGucuuGATT B	708
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	31380	MYC:1989L21 siRNA (1971C) stab05	ucAAGAcucAGccAAGGuuTsT	712
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	31383	MYC:1971U21 siRNA stab07	B *AA*ccuu*GG*cu*GA*Gucuu*GA*TT B	721
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	31386	MYC:1989L21 siRNA (1971C) stab11	uc*AAGA*cuc*AG*cc*AAGG*uuTsT	722
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	31389	MYC:1971U21 siRNA inv stab04	B AGuucuGAGucGGuuccAATT B	723
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	31392	MYC:1989L21 siRNA (1971C) inv stab05	uuGGAAccGAcucAGAAcuTsT	724

WO 03/074654 PCT/US03/05028

MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	sense	31395	MYC:1971U21 siRNA inv stab07	B *A*Guucu*GA*Guc*G*Guucc*AA*TT B	725
MYC	1969	ACAACCUUGGCUGAGUCUUGAGA	131	antisense	31398	MYC:1989L21 siRNA (1971C) inv stab11	uu*GGAA*cc*GA*cuc*AGAA*cuTsT	726
Nogo	1043	UCGUUCAGUGUCUCUCCAAAAGC	132	sense	30833	Nogo:1043U21 siRNA stab04	B GuucAGuGucucuccAAAATT B	727
Nogo	1407	GUUUUGCAGAUAGCCUUGAGCAA	133	sense	30834	Nogo:1407U21 siRNA stab04	B uuuGcAGAuAGccuuGAGcTT B	728
Nogo	3211	AUUCCUGCUGCUUUCAUUGACAG	134	sense	30835	Nogo:3211U21 siRNA stab04	B uccuGcuGcuuucAuuGAcTT B	729
Nogo	3883	UUGACUGCCAUGUGUUCAUCAUC	135	sense	30836	Nogo:3883U21 siRNA stab04	B GAcuGccAuGuGuucAucATT B	730
Nogo	1061	UCGUUCAGUGUCUCUCCAAAAGC	132	antisense	30837	Nogo:1061L21 siRNA (1043C) stab05	uuuuGGAGAGAcAcuGAAcTsT	731
Nogo	1425	GUUUUGCAGAUAGCCUUGAGCAA	133	antisense	30838	Nogo:1425L21 siRNA (1407C) stab05	GcucAAGGcuAucuGcAAATsT	732
Nogo	3229	AUUCCUGCUGCUUUCAUUGACAG	134	antisense	30839	Nogo:3229L21 siRNA (3211C) stab05	GucAAuGAAAGcAGcAGGATsT	733
Nogo	3901	UUGACUGCCAUGUGUUCAUCAUC	135	antisense	30840	Nogo:3901L21 siRNA (3883C) stab05	uGAuGAAcAcAuGGcAGucTsT	734
NOGO R	510	CCCUGCAGUACCUCUACCUGCAG	136	sense	31057	NogoR:512U21 siRNA	CUGCAGUACCUCUACCUGCTT	735
NOGO R	660	ACCGUCUCCUACUGCACCAGAAC	137	sense	31058	NogoR:662U21 siRNA	CGUCUCCUACUGCACCAGATT	736
NOGO R	1084	ACUGGAGCCUGGAAGACCAGCUU	138	sense	31059	NogoR:1086U21 siRNA	UGGAGCCUGGAAGACCAGCTT	737
NOGO R	1369	UGGUGACUCAGAAGGCUCAGGUG	139	sense	31060	NogoR:1371U21 siRNA	GUGACUCAGAAGGCUCAGGTT	738
NOGO R	510	CCCUGCAGUACCUCUACCUGCAG	136	antisense	31133	NogoR:530L21 siRNA (512C)	GCAGGUAGAGGUACUGCAGTT	739
NOGO R	660	ACCGUCUCCUACUGCACCAGAAC	137	antisense	31134	NogoR:680L21 siRNA (662C)	UCUGGUGCAGUAGGAGACGTT	740
NOGO R	1084	ACUGGAGCCUGGAAGACCAGCUU	138	antisense	31135	NogoR:1104L21 siRNA (1086C)	GCUGGUCUUCCAGGCUCCATT	741
NOGO R	1369	UGGUGACUCAGAAGGCUCAGGUG	139	antisense	31136	NogoR:1389L21 siRNA (1371C)	CCUGAGCCUUCUGAGUCACTT	742
PCNA	548	UUUGCACGUAUAUGCCGAGAUCU	140	sense	30841	PCNA:550U21 siRNA stab04	B uGcAcGuAuAuGccGAGAuTT B	743
PCNA	572	AGCCAUAUUGGAGAUGCUGUUGU	141	sense	30842	PCNA:574U21 siRNA stab04	B ccAuAuuGGAGAuGcuGuuTT B	744
PCNA	837	AAAUUGCGGAUAUGGGACACUUA	142	sense	30844	PCNA:839U21 siRNA stab04	B AuuGcGGAuAuGGGAcAcuTT B	745

WO 03/074654 PCT/US03/05028

(400/104)

PCNA	548	UUUGCACGUAUAUGCCGAGAUCU	140	antisense	30845	PCNA:568L21 siRNA (550C) stab05	AucucGGcAuAuAcGuGcATsT	746
PCNA	572	AGCCAUAUUGGAGAUGCUGUUGU	141	antisense	30846	PCNA:592L21 siRNA (574C) stab05	AAcAGcAucuccAAuAuGGTsT	747
PCNA	837	AAAUUGCGGAUAUGGGACACUUA	142	antisense	30848	PCNA:857L21 siRNA (839C) stab05	AGuGucccAuAuccGcAAuTsT	748
PCNA	548	UUUGCACGUAUAUGCCGAGAUCU	140	sense	31033	PCNA:550U21 siRNA	UGCACGUAUAUGCCGAGAUTT	749
PCNA	572	AGCCAUAUUGGAGAUGCUGUUGU	141	sense	31034	PCNA:574U21 siRNA	CCAUAUUGGAGAUGCUGUUTT	750
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	sense	31035	PCNA:767U21 siRNA	AAAGCCACUCCACUCUCUUTT	751
PCNA	837	AAAUUGCGGAUAUGGGACACUUA	142	sense	31036	PCNA:839U21 siRNA	AUUGCGGAUAUGGGACACUTT	752
PCNA	548	UUUGCACGUAUAUGCCGAGAUCU	140	antisense	31109	PCNA:568L21 siRNA (550C)	AUCUCGGCAUAUACGUGCATT	753
PCNA	572	AGCCAUAUUGGAGAUGCUGUUGU	141	antisense	31110	PCNA:592L21 siRNA (574C)	AACAGCAUCUCCAAUAUGGTT	754
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	antisense	31111	PCNA:785L21 siRNA (767C)	AAGAGAGUGGAGUGGCUUUTT	755
PCNA	837	AAAUUGCGGAUAUGGGACACUUA	142	antisense	31112	PCNA:857L21 siRNA (839C)	AGUGUCCCAUAUCCGCAAUTT	756
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	sense	31310	PCNA:767U21 siRNA stab04	B AAAGccAcuccAcucucuuTT B	757
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	antisense	31311	PCNA:785L21 siRNA (767C) stab05	AAGAGAGuGGAGuGGcuuuTsT	758
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	sense	31322	PCNA:767U21 siRNA inv stab04	B uucucucAccucAccGAAATT B	759
PCNA	765	CAAAAGCCACUCCACUCUCUUCA	143	antisense	31323	PCNA:785L21 siRNA (767C) inv stab05	uuucGGuGAGGuGAGAGAATsT	760
PKR	533	UUCAGGACCUCCACAUGAUAGGA	144	sense	30969	PKR:533U21 siRNA stab04	B cAGGAccuccAcAuGAuAGTT B	761
PKR	533	UUCAGGACCUCCACAUGAUAGGA	144	sense	30969	PKR:533U21 siRNA stab04	B cAGGAccuccAcAuGAuAGTT B	761
PKR	1171	AACAACCACAAAAUACAACAAGA	57	sense	30970	PKR:1171U21 siRNA stab04	B AGAuuuGAccuuccuGAcATT B	762
PKR	1171	AACAACCACAAAAUACAACAAGA	57	sense	30970	PKR:1171U21 siRNA stab04	B AGAuuuGAccuuccuGAcATT B	762
PKR	1171	AACAACCACAAAAUACAACAAGA	57	sense	30970	PKR:1171U21 siRNA stab04	B AGAuuuGAccuuccuGAcATT B	762
PKR	1171	AACAACCACAAAAUACAACAAGA	57	sense	30970	PKR:1171U21 siRNA stab04	B AGAuuuGAccuuccuGAcATT B	762
PKR	2430	AACAACCACAAAAUACAACAAGA	57	sense	30971	PKR:2430U21 siRNA stab04	B uGAGuAGcuGGAuuAcAGGTT B	763
PKR	2430	AACAACCACAAAAUACAACAAGA	57	sense	30971	PKR:2430U21 siRNA stab04	B uGAGuAGcuGGAuuAcAGGTT B	763

PKR	2518	AACAACCACAAAAUACAACAAGA	57	sense	30972	PKR:2518U21 siRNA stab04	B GGucucAAAcuccuGAccuTT B	764
PKR	2518	AACAACCACAAAAUACAACAAGA	57	sense	30972	PKR:2518U21 siRNA stab04	B GGucucAAAcuccuGAccuTT B	764
PKR	551	AACAACCACAAAAUACAACAAGA	57	antisense	30973	PKR:551L21 siRNA (533C) stab05	cuAucAuGuGGAGGuccuGTsT	765
PKR	551	AACAACCACAAAAUACAACAAGA	57	antisense	30973	PKR:551L21 siRNA (533C) stab05	cuAucAuGuGGAGGuccuGTsT	765
PKR	1189	AACAACCACAAAAUACAACAAGA	57	antisense	30974	PKR:1189L21 siRNA (1171C) stab05	uGucAGGAAGGucAAAucuTsT	766
PKR	1189	AACAACCACAAAAUACAACAAGA	57	antisense	30974	PKR:1189L21 siRNA (1171C) stab05	uGucAGGAAGGucAAAucuTsT	766
PKR	2448	AACAACCACAAAAUACAACAAGA	57	antisense	30975	PKR:2448L21 siRNA (2430C) stab05	ccuGuAAuccAGcuAcucATsT	767
PKR	2448	AACAACCACAAAAUACAACAAGA	57	antisense	30975	PKR:2448L21 siRNA (2430C) stab05	ccuGuAAuccAGcuAcucATsT	767
PKR	2536	AACAACCACAAAAUACAACAAGA	57	antisense	30976	PKR:2536L21 siRNA (2518C) stab05	AGGucAGGAGuuuGAGAccTsT	768
PKR	2536	AACAACCACAAAAUACAACAAGA	57	antisense	30976	PKR:2536L21 siRNA (2518C) stab05	AGGucAGGAGuuuGAGAccTsT	768
PRKCA	517	CUAAAGGCUGAGGUUGCUGAUGA	145	sense	30713	PRKCA:519U21 siRNA stab04	B AAAGGcuGAGGuuGcuGAuTT B	769
PRKCA	998	GGAAACAACCUUCCAACAACCUU	146	sense	30714	PRKCA:1000U21 siRNA stab04	B AAAcAAccuuccAAcAAccTT B	770
PRKCA	1734	CAAAGGACUGAUGACCAAACACC	147	sense	30716	PRKCA:1736U21 siRNA stab04	B AAGGAcuGAuGAccAAAcATT B	771
PRKCA	517	CUAAAGGCUGAGGUUGCUGAUGA	145	antisense	30717	PRKCA:537L21 siRNA (519C) stab05	AucAGcAAccucAGccuuuTsT	772
PRKCA	998	GGAAACAACCUUCCAACAACCUU	146	antisense	30718	PRKCA:1018L21 siRNA (1000C) stab05	GGuuGuuGGAAGGuuGuuuTsT	773
PRKCA	1734	CAAAGGACUGAUGACCAAACACC	147	antisense	30720	PRKCA:1754L21 siRNA (1736C) stab05	uGuuuGGucAucAGuccuuTsT	774
PRKCA	517	CUAAAGGCUGAGGUUGCUGAUGA	145	sense	30989	PRKCA:519U21 siRNA	AAAGGCUGAGGUUGCUGAUTT	775
PRKCA	998	GGAAACAACCUUCCAACAACCUU	146	sense	30990	PRKCA:1000U21 siRNA	AAACAACCUUCCAACAACCTT	776
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	sense	30991	PRKCA:1143U21 siRNA	GGAUGUGGUGAUUCAGGAUTT	777
PRKCA	1734	CAAAGGACUGAUGACCAAACACC	147	sense	30992	PRKCA:1736U21 siRNA	AAGGACUGAUGACCAAACATT	778
PRKCA	517	CUAAAGGCUGAGGUUGCUGAUGA	145	antisense	31065	PRKCA:537L21 siRNA (519C)	AUCAGCAACCUCAGCCUUUTT	779
PRKCA	998	GGAAACAACCUUCCAACAACCUU	146	antisense	31066	PRKCA:1018L21 siRNA (1000C)	GGUUGUUGGAAGGUUGUUUTT	780
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	antisense	31067	PRKCA:1161L21 siRNA (1143C)	AUCCUGAAUCACCACAUCCTT	781

PRKCA	1734	CAAAGGACUGAUGACCAAACACC	147	antisense	31068	PRKCA:1754L21 siRNA (1736C)	UGUUUGGUCAUCAGUCCUUTT	782
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	sense	31376	PRKCA:1143U21 siRNA stab04	B GGAuGuGGuGAuucAGGAuTT B	783
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	antisense	31379	PRKCA:1161L21 siRNA (1143C) stab05	AuccuGAAucAccAcAuccTsT	784
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	sense	31382	PRKCA:1143U21 siRNA stab07	B *GGAuGuGGuGAuucAGGAuTT* B	785
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	antisense	31385	PRKCA:1161L21 siRNA (1143C) stab11	*A*uccu*GAAucAccAcAuccTsT*	786
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	sense	31388	PRKCA:1143U21 siRNA inv stab04	B uAGGAcuuAGuGGuGuAGGTT B	787
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	antisense	31391	PRKCA:1161L21 siRNA (1143C) inv stab05	ccuAcAccAcuAAGuccuATsT	788
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	sense	31394	PRKCA:1143U21 siRNA inv stab07	B u*AGGAcuuAGuGGuGuAGGTT* B	789
PRKCA	1141	AAGGAUGUGGUGAUUCAGGAUGA	148	antisense	31397	PRKCA:1161L21 siRNA (1143C) inv stab11	ccu*AcAccAcuAAGuccuATsT*	790
PTP4A3	205	AUCUCGUUUCUCUUGGACAAGCA	149	sense	31557	PTP4A3:205U21 siRNA	CUCGUUUCUCUUGGACAAGTT	791
PTP4A3	367	GAGGUGAGCUACAAACACAUGCG	150	sense	31558	PTP4A3:367U21 siRNA	GGUGAGCUACAAACACAUGTT	792
PTP4A3	574	GUAGUGGAAGACUGGCUGAGCCU	151	sense	31559	PTP4A3:574U21 siRNA	AGUGGAAGACUGGCUGAGCTT	793
PTP4A3	1168	CUCCUCUAGCCUGUUUGUUGUGG	152	sense	31560	PTP4A3:1168U21 siRNA	CCUCUAGCCUGUUUGUUGUTT	794
PTP4A3	223	AUCUCGUUUCUCUUGGACAAGCA	149	antisense	31561	PTP4A3:223L21 siRNA (205C)	CUUGUCCAAGAGAAACGAGTT	795
PTP4A3	385	GAGGUGAGCUACAAACACAUGCG	150	antisense	31562	PTP4A3:385L21 siRNA (367C)	CAUGUGUUUGUAGCUCACCTT	796
PTP4A3	592	GUAGUGGAAGACUGGCUGAGCCU	151	antisense	31563	PTP4A3:592L21 siRNA (574C)	GCUCAGCCAGUCUUCCACUTT	797
PTP4A3	1186	CUCCUCUAGCCUGUUUGUUGUGG	152	antisense	31564	PTP4A3:1186L21 siRNA (1168C)	ACAACAAACAGGCUAGAGGTT	798
PTPN1	240	UAUCCGACAUGAAGCCAGUGACU	153	sense	30865	PTPN1:242U21 siRNA stab04	B uccGAcAuGAAGccAGuGATT B	799
PTPN1	872	UGCUGAUGGACAAGAGGAAAGAC	154	sense	30867	PTPN1:874U21 siRNA stab04	B cuGAuGGAcAAGAGGAAAGTT B	800
PTPN1	3035	AGGUGUGGAUAAGGCUUAGGUGC	155	sense	30868	PTPN1:3037U21 siRNA stab04	B GuGuGGAuAAGGcuuAGGuTT B	801
PTPN1	240	UAUCCGACAUGAAGCCAGUGACU	153	antisense	30869	PTPN1:260L21 siRNA (242C) stab05	ucAcuGGcuucAuGucGGATsT	802

WO 03/074654 PCT/US03/05028

PTPN1	872	UGCUGAUGGACAAGAGGAAAGAC	154	antisense	30871	PTPN1:892L21 siRNA (874C) stab05	cuuuccucuuGuccAucAGTsT	803
PTPN1	3035	AGGUGUGGAUAAGGCUUAGGUGC	155	antisense	30872	PTPN1:3055L21 siRNA (3037C) stab05	AccuAAGccuuAuccAcAcTsT	804
PTPN1	240	UAUCCGACAUGAAGCCAGUGACU	153	sense	31017	PTPN1:242U21 siRNA	UCCGACAUGAAGCCAGUGATT	805
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	sense	31018	PTPN1:766U21 siRNA	GUCCGAGAGUCAGGGUCACTT	806
PTPN1	872	UGCUGAUGGACAAGAGGAAAGAC	154	sense	31019	PTPN1:874U21 siRNA	CUGAUGGACAAGAGGAAAGTT	807
PTPN1	3035	AGGUGUGGAUAAGGCUUAGGUGC	155	sense	31020	PTPN1:3037U21 siRNA	GUGUGGAUAAGGCUUAGGUTT	808
PTPN1	240	UAUCCGACAUGAAGCCAGUGACU	153	antisense	31093	PTPN1:260L21 siRNA (242C)	UCACUGGCUUCAUGUCGGATT	809
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	antisense	31094	PTPN1:784L21 siRNA (766C)	GUGACCCUGACUCUCGGACTT	810
PTPN1	872	UGCUGAUGGACAAGAGGAAAGAC	154	antisense	31095	PTPN1:892L21 siRNA (874C)	CUUUCCUCUUGUCCAUCAGTT	811
PTPN1	3035	AGGUGUGGAUAAGGCUUAGGUGC	155	antisense	31096	PTPN1:3055L21 siRNA (3037C)	ACCUAAGCCUUAUCCACACTT	812
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	sense	31306	PTPN1:766U21 siRNA stab04	B GuccGAGAGucAGGGucAcTT B	813
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	antisense	31307	PTPN1:784L21 siRNA (766C) stab05	GuGAcccuGAcucucGGAcTsT	814
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	sense	31318	PTPN1:766U21 siRNA inv stab04	B cAcuGGGAcuGAGAGccuGTT B	815
PTPN1	764	AAGUCCGAGAGUCAGGGUCACUC	156	antisense	31319	PTPN1:784L21 siRNA (766C) inv stab05	cAGGcucucAGucccAGuGTsT	816
RAF1	1326	AAAACACGGCAUGUGAACAUUCU	157	sense	31549	RAF1:1326U21 siRNA	AACACGGCAUGUGAACAUUTT	817
RAF1	1415	CCUCUACAAACACCUGCAUGUCC	158	sense	31550	RAF1:1415U21 siRNA	UCUACAAACACCUGCAUGUTT	818
RAF1	1776	UCUCACAUCAACAACCGAGAUCA	159	sense	31551	RAF1:1776U21 siRNA	UCACAUCAACAACCGAGAUTT	819
RAF1	2854	CAAGGAAGCCAGGAAUACAGGUU	160	sense	31552	RAF1:2854U21 siRNA	AGGAAGCCAGGAAUACAGGTT	820
RAF1	1344	AAAACACGGCAUGUGAACAUUCU	157	antisense	31553	RAF1:1344L21 siRNA (1326C)	AAUGUUCACAUGCCGUGUUTT	821
RAF1	1433	CCUCUACAAACACCUGCAUGUCC	158	antisense	31554	RAF1:1433L21 siRNA (1415C)	ACAUGCAGGUGUUUGUAGATT	822
RAF1	1794	UCUCACAUCAACAACCGAGAUCA	159	antisense	31555	RAF1:1794L21 siRNA (1776C)	AUCUCGGUUGUUGAUGUGATT	823
RAF1	2872	CAAGGAAGCCAGGAAUACAGGUU	160	antisense	31556	RAF1:2872L21 siRNA (2854C)	CCUGUAUUCCUGGCUUCCUTT	824
RELA	144	GAGAGGAGCACAGAUACCACCAA	161	sense	31029	RelA:146U21 siRNA	GAGGAGCACAGAUACCACCTT	825
RELA	288	GAUGGCUUCUAUGAGGCUGAGCU	162	sense	31030	RelA:290U21 siRNA	UGGCUUCUAUGAGGCUGAGTT	826
RELA	643	UGUGUGACAAGGUGCAGAAAGAG	163	sense	31031	RelA:645U21 siRNA	UGUGACAAGGUGCAGAAAGTT	827
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	sense	31032	RelA:1957U21 siRNA	CUCCAGCUUCUGGUACUCUTT	828
RELA	144	GAGAGGAGCACAGAUACCACCAA	161	antisense	31105	RelA:164L21 siRNA	GGUGGUAUCUGUGCUCCUCTT	829

						(146C)		
RELA	288	GAUGGCUUCUAUGAGGCUGAGCU	162	antisense	31106	RelA:308L21 siRNA (290C)	CUCAGCCUCAUAGAAGCCATT	830
RELA	643	UGUGUGACAAGGUGCAGAAAGAG	163	antisense	31107	RelA:663L21 siRNA (645C)	CUUUCUGCACCUUGUCACATT	831
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	antisense	31108	RelA:1975L21 siRNA (1957C)	AGAGUACCAGAAGCUGGAGTT	832
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	sense	31308	RelA:1957U21 siRNA stab04	B cuccAGcuucuGGuAcucuTT B	833
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	antisense	31309	RelA:1975L21 siRNA (1957C) stab05	AGAGuAccAGAAGcuGGAGTsT	834
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	sense	31320	RELA:1957U21 siRNA inv stab04	B ucucAuGGucuucGAccucTT B	835
RELA	1955	UCCUCCAGCUUCUGGUACUCUCC	164	antisense	31321	RELA:1975L21 siRNA (1957C) inv stab05	GAGGucGAAGAccAuGAGATsT	836
SCD	993	GAUAUGCUGUGGUGCUUAAUGCC	165	sense	30873	SCD:995U21 siRNA stab04	B uAuGcuGuGGuGcuuAAuGTT B	837
SCD	2518	ACUGCUGGACAUGAGAUGGAGAG	166	sense	30874	SCD:2520U21 siRNA stab04	B uGcuGGAcAuGAGAuGGAGTT B	838
SCD	3783	UAGAGGCUACAGGGGUUAGCCUG	167	sense	30875	SCD:3785U21 siRNA stab04	B GAGGcuAcAGGGGuuAGccTT B	839
SCD	4772	CUGACCUACCUCAAAGGGCAGUU	168	sense	30876	SCD:4774U21 siRNA stab04	B GAccuAccucAAAGGGcAGTT B	840
SCD	993	GAUAUGCUGUGGUGCUUAAUGCC	165	antisense	30877	SCD:1013L21 siRNA (995C) stab05	cAuuAAGcAccAcAGcAuATsT	841
SCD	2518	ACUGCUGGACAUGAGAUGGAGAG	166	antisense	30878	SCD:2538L21 siRNA (2520C) stab05	cuccAucucAuGuccAGcATsT	842
SCD	3783	UAGAGGCUACAGGGGUUAGCCUG	167	antisense	30879	SCD:3803L21 siRNA (3785C) stab05	GGcuAAccccuGuAGccucTsT	843
SCD	4772	CUGACCUACCUCAAAGGGCAGUU	168	antisense	30880	SCD:4792L21 siRNA (4774C) stab05	cuGcccuuuGAGGuAGGucTsT	844
SCD	993	GAUAUGCUGUGGUGCUUAAUGCC	165	sense	31021	SCD:995U21 siRNA	UAUGCUGUGGUGCUUAAUGTT	845
SCD	2518	ACUGCUGGACAUGAGAUGGAGAG	166	sense	31022	SCD:2520U21 siRNA	UGCUGGACAUGAGAUGGAGTT	846
SCD	3783	UAGAGGCUACAGGGGUUAGCCUG	167	sense	31023	SCD:3785U21 siRNA	GAGGCUACAGGGGUUAGCCTT	847
SCD	4772	CUGACCUACCUCAAAGGGCAGUU	168	sense	31024	SCD:4774U21 siRNA	GACCUACCUCAAAGGGCAGTT	848
SCD	993	GAUAUGCUGUGGUGCUUAAUGCC	165	antisense	31097	SCD:1013L21 siRNA (995C)	CAUUAAGCACCACAGCAUATT	849
SCD	2518	ACUGCUGGACAUGAGAUGGAGAG	166	antisense	31098	SCD:2538L21 siRNA (2520C)	CUCCAUCUCAUGUCCAGCATT	850
SCD	3783	UAGAGGCUACAGGGGUUAGCCUG	167	antisense	31099	SCD:3803L21 siRNA (3785C)	GGCUAACCCCUGUAGCCUCTT	851

SCD	4772	CUGACCUACCUCAAAGGGCAGUU	168	antisense	31100	SCD:4792L21 siRNA (4774C)	CUGCCCUUUGAGGUAGGUCTT	852
TERT	17	CUGCGCACGUGGGAAGCCCUGGC	169	sense	29960	TERT:19U21 siRNA	GCGCACGUGGGAAGCCCUGGC	853
TERT	309	UGCAGAGGCUGUGCGAGCGCGGC	170	sense	29961	TERT:311U21 siRNA	CAGAGGCUGUGCGAGCGCGGC	854
TERT	641	CGUCUGGGAUGCGAACGGGCCUG	171	sense	29962	TERT:643U21 siRNA	UCUGGGAUGCGAACGGGCCUG	855
TERT	1244	CUUGGGAACCACGCGCAGUGCCC	172	sense	29963	TERT:1246U21 siRNA	UGGGAACCACGCGCAGUGCCC	856
TERT	2495	UGCCACCACGCCGUGCGCAUCAG	173	sense	29964	TERT:2497U21 siRNA	CCACCACGCCGUGCGCAUCAG	857
TERT	17	CUGCGCACGUGGGAAGCCCUGGC	169	antisense	29965	TERT:39L21 siRNA (19C)	CAGGGCUUCCCACGUGCGCAG	858
TERT	309	UGCAGAGGCUGUGCGAGCGCGGC	170	antisense	29966	TERT:331L21 siRNA (311C)	CGCGCUCGCACAGCCUCUGCA	859
TERT	641	CGUCUGGGAUGCGAACGGGCCUG	171	antisense	29967	TERT:663L21 siRNA (643C)	GGCCCGUUCGCAUCCCAGACG	860
TERT	1244	CUUGGGAACCACGCGCAGUGCCC	172	antisense	29968	TERT:1266L21 siRNA (1246C)	GCACUGCGCGUGGUUCCCAAG	861
TERT	2495	UGCCACCACGCCGUGCGCAUCAG	173	antisense	29969	TERT:2517L21 siRNA (2497C)	GAUGCGCACGGCGUGGUGGCA	862
TERT	1136	GUGGAGACCAUCUUUCUGGGUUC	174	sense	30905	TERT:1138U21 siRNA stab04	B GGAGAccAucuuucuGGGuTT B	863
TERT	1790	AGUGUCUGGAGCAAGUUGCAAAG	175	sense	30906	TERT:1792U21 siRNA stab04	B uGucuGGAGcAAGuuGcAATT B	864
TERT	2915	AUCAGAGCCAGUCUCACCUUCAA	176	sense	30907	TERT:2917U21 siRNA stab04	B cAGAGccAGucucAccuucTT B	865
TERT	2994	UGAAGUGUCACAGCCUGUUUCUG	177	sense	30908	TERT:2996U21 siRNA stab04	B AAGuGucAcAGccuGuuucTT B	866
TERT	1136	GUGGAGACCAUCUUUCUGGGUUC	174	antisense	30909	TERT:1156L21 siRNA (1138C) stab05	AcccAGAAAGAuGGucuccTsT	867
TERT	1790	AGUGUCUGGAGCAAGUUGCAAAG	175	antisense	30910	TERT:1810L21 siRNA (1792C) stab05	uuGcAAcuuGcuccAGAcATsT	868
TERT	2915	AUCAGAGCCAGUCUCACCUUCAA	176	antisense	30911	TERT:2935L21 siRNA (2917C) stab05	GAAGGuGAGAcuGGcucuGTsT	869
TERT	2994	UGAAGUGUCACAGCCUGUUUCUG	177	antisense	30912	TERT:3014L21 siRNA (2996C) stab05	GAAAcAGGcuGuGAcAcuuTsT	870
TGFB1	1526	AGGGAUAACACACUGCAAGUGGA	178	sense	30881	TGFb:1528U21 siRNA stab04	B GGAuAAcAcAcuGcAAGuGTT B	871
TGFB1	2383	CCAUAGCAACACUCUGAGAUGGC	179	sense	30882	TGFb:2385U21 siRNA stab04	B AuAGcAAcAcucuGAGAuGTT B	872
TGFB1	2484	GAACCUGCUUUAGUGGGGGAUAG	180	sense	30883	TGFb:2486U21 siRNA stab04	B AccuGcuuuAGuGGGGGAuTT B	873
TGFB1	2566	UAGCACUUUUGGGAGGCAGAGAU	181	sense	30884	TGFb:2568U21 siRNA stab04	B GcAcuuuuGGGAGGcAGAGTT B	874
TGFB1	1526	AGGGAUAACACACUGCAAGUGGA	178	antisense	30885	TGFb:1546L21 siRNA	cAcuuGcAGuGuGuuAuccTsT	875

						(1528C) stab05		
TGFB1	2383	CCAUAGCAACACUCUGAGAUGGC	179	antisense	30886	TGFb:2403L21 siRNA (2385C) stab05	cAucucAGAGuGuuGcuAuTsT	876
TGFB1	2484	GAACCUGCUUUAGUGGGGGAUAG	180	antisense	30887	TGFb:2504L21 siRNA (2486C) stab05	AucccccAcuAAAGcAGGuTsT	877
TGFB1	2566	UAGCACUUUUGGGAGGCAGAGAU	181	antisense	30888	TGFb:2586L21 siRNA (2568C) stab05	cucuGccucccAAAAGuGcTsT	878
TGFB1	1526	AGGGAUAACACACUGCAAGUGGA	178	sense	31053	TGFb:1528U21 siRNA	GGAUAACACACUGCAAGUGTT	879
TGFB1	2383	CCAUAGCAACACUCUGAGAUGGC	179	sense	31054	TGFb:2385U21 siRNA	AUAGCAACACUCUGAGAUGTT	880
TGFB1	2484	GAACCUGCUUUAGUGGGGGAUAG	180	sense	31055	TGFb:2486U21 siRNA	ACCUGCUUUAGUGGGGGAUTT	881
TGFB1	2566	UAGCACUUUUGGGAGGCAGAGAU	181	sense	31056	TGFb:2568U21 siRNA	GCACUUUUGGGAGGCAGAGTT	882
TGFB1	1526	AGGGAUAACACACUGCAAGUGGA	178	antisense	31129	TGFb:1546L21 siRNA (1528C)	CACUUGCAGUGUGUUAUCCTT	883
TGFB1	2383	CCAUAGCAACACUCUGAGAUGGC	179	antisense	31130	TGFb:2403L21 siRNA (2385C)	CAUCUCAGAGUGUUGCUAUTT	884
TGFB1	2484	GAACCUGCUUUAGUGGGGGAUAG	180	antisense	31131	TGFb:2504L21 siRNA (2486C)	AUCCCCCACUAAAGCAGGUTT	885
TGFB1	2566	UAGCACUUUUGGGAGGCAGAGAU	181	antisense	31132	TGFb:2586L21 siRNA (2568C)	CUCUGCCUCCCAAAAGUGCTT	886
TNF	77	AAGGACACCAUGAGCACUGAAAG	182	sense	30889	TNFa:79U21 siRNA stab04	B GGAcAccAuGAGcAcuGAATT B	887
TNF	176	UUGUUCCUCAGCCUCUUCUCCUU	183	sense	30890	TNFa:178U21 siRNA stab04	B GuuccucAGccucuucuccTT B	888
TNF	568	CUCCUACCAGACCAAGGUCAACC	184	sense	30891	TNFa:570U21 siRNA stab04	B ccuAccAGAccAAGGucAATT B	889
TNF	1150	UUAGGCCUUCCUCUCUCCAGAUG	185	sense	30892	TNFa:1152U21 siRNA stab04	B AGGccuuccucucuccAGATT B	890
TNF	77	AAGGACACCAUGAGCACUGAAAG	182	antisense	30893	TNFa:97L21 siRNA (79C) stab05	uucAGuGcucAuGGuGuccTsT	891
TNF	176	UUGUUCCUCAGCCUCUUCUCCUU	183	antisense	30894	TNFa:196L21 siRNA (178C) stab05	GGAGAAGAGGcuGAGGAAcTsT	892
TNF	568	CUCCUACCAGACCAAGGUCAACC	184	antisense	30895	TNFa:588L21 siRNA (570C) stab05	uuGAccuuGGucuGGuAGGTsT	893
TNF	1150	UUAGGCCUUCCUCUCUCCAGAUG	185	antisense	30896	TNFa:1170L21 siRNA (1152C) stab05	ucuGGAGAGAGGAAGGccuTsT	894
TNF	77	AAGGACACCAUGAGCACUGAAAG	182	sense	31408	TNFa:79U21 siRNA	GGACACCAUGAGCACUGAATT	895
TNF	176	UUGUUCCUCAGCCUCUUCUCCUU	183	sense	31409	TNFa:178U21 siRNA	GUUCCUCAGCCUCUUCUCCTT	896
TNF	568	CUCCUACCAGACCAAGGUCAACC	184	sense	31410	TNFa:570U21 siRNA	CCUACCAGACCAAGGUCAATT	897
TNF	1150	UUAGGCCUUCCUCUCUCCAGAUG	185	sense	31411	TNFa:1152U21 siRNA	AGGCCUUCCUCUCUCCAGATT	898
TNF	77	AAGGACACCAUGAGCACUGAAAG	182	antisense	31412	TNFa:97L21 siRNA (79C)	UUCAGUGCUCAUGGUGUCCTT	899

TNF	176	UUGUUCCUCAGCCUCUUCUCCUU	183	antisense	31413	TNFa:196L21 siRNA (178C)	GGAGAAGAGGCUGAGGAACTT	900
TNF	568	CUCCUACCAGACCAAGGUCAACC	184	antisense	31414	TNFa:588L21 siRNA (570C)	UUGACCUUGGUCUGGUAGGTT	901
TNF	1150	UUAGGCCUUCCUCUCUCCAGAUG	185	antisense	31415	TNFa:1170L21 siRNA (1152C)	UCUGGAGAGAGGAAGGCCUTT	902

Uppercase = ribonucleotide
u,c = 2'-deoxy-2'-fluoro U,C
T = thymidine
B = inverted deoxy abasic
s = phosphorothioate linkage
A = deoxy Adenosine
G = deoxy Guanosine

WO 03/074654 PCT/US03/05028

Table II

A. 2.5 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 µL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 µL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 µL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 µL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 µL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 µL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 µL	5 sec	5 sec	5 sec
TCA	700	732 µL	10 sec	10 sec	10 sec
Iodine	20.6	244 µL	15 sec	15 sec	15 sec
Beaucage	7.7	232 µL	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 µmol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O-methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 µL	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 µL	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 µL	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 µL	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 µL	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 µL	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 µL	NA	NA	NA

- Wait time does not include contact time during delivery.
- Tandem synthesis utilizes double coupling of linker molecule

Table III

Group	Solution on Filter (1.0 µL)	Stock VEGF concentration	Number of Animals	Injectate (6.0 µL)	Dose	Conc. injectate
1	Tris-Cl pH 6.9	NA	5	water	NA	NA
2	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	water	NA	NA
3	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Site 2340 Stab1 siRNA	10 µg/eye	1.67 µg/µL
4	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Site 2340 Stab1 siRNA	3 µg/eye	0.5 µg/µL
5	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Site 2340 Stab1 siRNA	1 µg/eye	0.167 µg/µL
6	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Inactive Site 2340 Stab1 siRNA	10 µg/eye	1.67 µg/µL
7	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Inactive Site 2340 Stab1 siRNA	3 µg/eye	0.5 µg/µL
8	R&D Systems VEGF-carrier free 75 µM	3.53 µg/µL	5	Inactive Site 2340 Stab1 siRNA	1 µg/eye	0.167 µg/µL

Table IV

Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	Purine	cap	p=S	Strand
"Stab 1"	Ribo	Ribo	-	5 at 5'-end 1 at 3'-end	S/AS
"Stab 2"	Ribo	Ribo	-	All linkages	Usually AS
"Stab 3"	2'-fluoro	Ribo	-	4 at 5'-end 4 at 3'-end	Usually S
"Stab 4"	2'-fluoro	Ribo	5' and 3'-ends	-	Usually S
"Stab 5"	2'-fluoro	Ribo	-	1 at 3'-end	Usually AS
"Stab 6"	2'-O-Methyl	Ribo	5' and 3'-ends	-	Usually S
"Stab 7"	2'-fluoro	2'-deoxy	5' and 3'-ends	-	Usually S
"Stab 8"	2'-fluoro	2'-O-Methyl	-	1 at 3'-end	Usually AS
"Stab 9"	Ribo	Ribo	5' and 3'-ends	-	Usually S
"Stab 10"	Ribo	Ribo	-	1 at 3'-end	Usually AS
"Stab 11"	2'-fluoro	2'-deoxy	-	1 at 3'-end	Usually AS

CAP = any terminal cap, see for example **Figure 10**.

All Stab 1-11 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 1-11 chemistries typically comprise 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V

Acc#	Description
NM_002825	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
NM_033418	Homo sapiens hypothetical protein MGC9084 (MGC9084), mRNA
NM_033111	Homo sapiens LOC88523 (LOC88523), mRNA
NM_032564	Homo sapiens diacylglycerol O-acyltransferase homolog 2 (mouse) (DGAT2), mRNA
NM_032311	Homo sapiens KIAA1649 protein (KIAA1649), mRNA
NM_022130	Homo sapiens golgi phosphoprotein 3 (coat-protein) (GOLPH3), mRNA
NM_021980	Homo sapiens optineurin (OPTN), mRNA
NM_000660	Homo sapiens transforming growth factor, beta 1 (Camurati-Engelmann disease) (TGFB1), mRNA
NM_020423	Homo sapiens hypothetical protein LOC57147 (LOC57147), mRNA
NM_020351	Homo sapiens smooth muscle cell-expressed and macrophage conditioned medium-induced protein smag-64 (LOC57086), mRNA
NM_019556	Homo sapiens hypothetical protein dJ473B4 (DJ473B4), mRNA
NM_018676	Homo sapiens TMTSP for transmembrane molecule with thrombospondin module (LOC55901), mRNA
NM_016265	Homo sapiens GIOT-3 for gonadotropin inducible transcription repressor-3 (GIOT-3), mRNA
NM_016531	Homo sapiens Kruppel-like factor 3 (basic) (KLF3), mRNA
NM_016372	Homo sapiens seven transmembrane domain orphan receptor (TPRA40), mRNA
NM_016211	Homo sapiens yeast Sec31p homolog (KIAA0905), mRNA
NM_014933	Homo sapiens yeast Sec31p homolog (KIAA0905), mRNA
NM_014706	Homo sapiens squamous cell carcinoma antigen recognised by T cells 3 (SART3), mRNA
NM_014463	Homo sapiens Lsm3 protein (LSM3), mRNA
NM_014288	Homo sapiens integrin beta 3 binding protein (beta3-endonexin) (ITGB3BP), mRNA
NM_013443	Homo sapiens CMP-NeuAC:(beta)-N-acetylgalactosaminide (alpha)2,6-sialyltransferase member VI (VI), mRNA
NM_012404	Homo sapiens pp32 related 2 (PP32R2), mRNA
NM_012403	Homo sapiens pp32 related 1 (PP32R1), mRNA
NM_006710	Homo sapiens COP9 homolog (COP9), mRNA
NM_006117	Homo sapiens peroxisomal D3,D2-enoyl-CoA isomerase (PECI), mRNA
NM_005839	Homo sapiens serine/arginine repetitive matrix 1 (SRRM1), mRNA
NM_004264	Homo sapiens SRB7 suppressor of RNA polymerase B homolog (yeast) (SURB7), mRNA
NM_003714	Homo sapiens stanniocalcin 2 (STC2), mRNA
NM_003122	Homo sapiens serine protease inhibitor, Kazal type 1 (SPINK1), mRNA
NM_003690	Homo sapiens protein kinase, interferon-inducible double stranded RNA dependent activator (PRKRA), mRNA
NM_015526	Homo sapiens CLIP-170-related protein (CLIPR-59), mRNA
NM_033401	Homo sapiens cell recognition protein CASPR4 (CASPR4), mRNA
NM_023037	Homo sapiens hypothetical protein CG003 (13CDNA73), mRNA
NM_021817	Homo sapiens brain link protein-1 (BRAL1), mRNA
NM_016222	Homo sapiens DEAD-box protein abstrakt (ABS), mRNA
NM_003744	Homo sapiens numb homolog (Drosophila) (NUMB), mRNA
NM_032682	Homo sapiens forkhead box P1 (FOXP1), mRNA
NM_003681	Homo sapiens pyridoxal (pyridoxine, vitamin B6) kinase (PDXK), mRNA

NM_001685	Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6 (ATP5J), mRNA
NM_017954	Homo sapiens hypothetical protein FLJ20761 (FLJ20761), mRNA
NM_015626	Homo sapiens SOCS box-containing WD protein SWiP-1 (WSB1), mRNA
NM_130795	Homo sapiens regulator of G-protein signalling 3 (RGS3), mRNA
NM_030877	Homo sapiens chromosome 20 open reading frame 33 (C20orf33), mRNA
NM_080830	Homo sapiens cystatin 11 (CST11), mRNA
NM_032329	Homo sapiens p28 ING5 (ING5), mRNA
NM_022917	Homo sapiens nucleolar RNA-associated protein (Nrap), mRNA
NM_130787	Homo sapiens adaptor-related protein complex 2, alpha 1 subunit (AP2A1), mRNA
NM_024744	Homo sapiens (ALS2CR8), mRNA
NM_018984	Homo sapiens slingshot 1 (hSSH-1), mRNA
NM_106552	Homo sapiens hypothetical protein FLJ14249 similar to HS1 binding protein 3 (FLJ14249), transcript variant 2, mRNA
NM_022460	Homo sapiens hypothetical protein FLJ14249 similar to HS1 binding protein 3 (FLJ14249), transcript variant 1, mRNA
NM_130446	Homo sapiens kelch-like protein KLHL6 (KLHL6), mRNA
NM_020314	Homo sapiens esophageal cancer associated protein (MGC16824), mRNA
NM_130395	Homo sapiens Werner helicase interacting protein (WHIP), transcript variant 2, mRNA
NM_020135	Homo sapiens Werner helicase interacting protein (WHIP), transcript variant 1, mRNA
NM_130388	Homo sapiens ankyrin repeat and SOCS box-containing 12 (ASB12), mRNA
NM_130387	Homo sapiens ankyrin repeat and SOCS box-containing 14 (ASB14), mRNA
NM_007191	Homo sapiens WNT inhibitory factor 1 (WIF1), mRNA
NM_052950	Homo sapiens WD40- and FYVE-domain containing protein 2 (WDF2), mRNA
NM_025042	Homo sapiens Williams-Beuren syndrome chromosome region 23 (WBSCR23), mRNA
NM_080706	Homo sapiens transient receptor potential cation channel, subfamily V, member 1 (TRPV1), transcript variant 3, mRNA
NM_080705	Homo sapiens transient receptor potential cation channel, subfamily V, member 1 (TRPV1), transcript variant 4, mRNA
NM_080704	Homo sapiens transient receptor potential cation channel, subfamily V, member 1 (TRPV1), transcript variant 1, mRNA
NM_018727	Homo sapiens transient receptor potential cation channel, subfamily V, member 1 (TRPV1), transcript variant 2, mRNA
NM_080879	Homo sapiens SOCS box containing protein RAR2A (RAR2A), mRNA
NM_080871	Homo sapiens ankyrin repeat and SOCS box-containing 10 (ASB10), mRNA
NM_080870	Homo sapiens DPCR1 protein (DPCR1), mRNA
NM_080834	Homo sapiens chromosome 20 open reading frame 152 (C20orf152), mRNA
NM_080829	Homo sapiens chromosome 20 open reading frame 175 (C20orf175), mRNA
NM_080828	Homo sapiens chromosome 20 open reading frame 173 (C20orf173), mRNA
NM_080819	Homo sapiens G protein-coupled receptor 78 (GPR78), mRNA
NM_080752	Homo sapiens chromosome 20 open reading frame 164 (C20orf164), mRNA
NM_080749	Homo sapiens chromosome 20 open reading frame 163 (C20orf163), mRNA
NM_080745	Homo sapiens ring finger protein 36 (RNF36), mRNA
NM_080738	Homo sapiens EDAR-associated death domain (EDARADD), mRNA
NM_014970	Homo sapiens kinesin-associated protein 3 (KIFAP3), mRNA
NM_021058	Homo sapiens H2B histone family, member R (H2BFR), mRNA
NM_021064	Homo sapiens H2A histone family, member P (H2AFP), mRNA
NM_080491	Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 1,

	mRNA
NM_012296	Homo sapiens GRB2-associated binding protein 2 (GAB2), transcript variant 2, mRNA
NM_007247	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), transcript variant 1, mRNA
NM_080551	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), transcript variant 3, mRNA
NM_080550	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), transcript variant 2, mRNA
NM_000982	Homo sapiens ribosomal protein L21 (RPL21), mRNA
NM_003913	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
NM_002475	Homo sapiens myosin light chain 1 slow a (MLC1SA), mRNA
NM_002729	Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA
NM_005893	Homo sapiens calicin (CCIN), mRNA
NM_017593	Homo sapiens homolog of mouse BMP-2 inducible kinase (BIKE), mRNA
NM_032027	Homo sapiens beta-amyloid binding protein precursor (BBP), mRNA
NM_004051	Homo sapiens 3-hydroxybutyrate dehydrogenase (heart, mitochondrial) (BDH), nuclear gene encoding mitochondrial protein, mRNA
NM_006576	Homo sapiens advillin (AVIL), mRNA
NM_013375	Homo sapiens TATA-binding protein-binding protein (ABT1), mRNA
NM_058219	Homo sapiens homolog of yeast mRNA transport regulator 3 (MTR3), mRNA
NM_058237	Homo sapiens HEAT-like repeat-containing protein (KIAA1622), transcript variant 1, mRNA
NM_020958	Homo sapiens HEAT-like repeat-containing protein (KIAA1622), transcript variant 2, mRNA
NM_004702	Homo sapiens cyclin E2 (CCNE2), transcript variant 3, mRNA
NM_057749	Homo sapiens cyclin E2 (CCNE2), transcript variant 1, mRNA
NM_057735	Homo sapiens cyclin E2 (CCNE2), transcript variant 2, mRNA
NM_002013	Homo sapiens FK506 binding protein 3 (25kD) (FKBP3), mRNA
NM_004724	Homo sapiens ZW10 homolog, centromere/kinetochore protein (Drosophila) (ZW10), mRNA
NM_057159	Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 2, mRNA
NM_001401	Homo sapiens endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2 (EDG2), transcript variant 1, mRNA
NM_015084	Homo sapiens mitochondrial ribosomal protein S27 (MRPS27), nuclear gene encoding mitochondrial protein, mRNA
NM_033281	Homo sapiens mitochondrial ribosomal protein S36 (MRPS36), nuclear gene encoding mitochondrial protein, mRNA
NM_005830	Homo sapiens mitochondrial ribosomal protein S31 (MRPS31), nuclear gene encoding mitochondrial protein, mRNA
NM_012062	Homo sapiens dynamin 1-like (DNM1L), transcript variant 1, mRNA
NM_005648	Homo sapiens transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C) (TCEB1), mRNA
NM_007070	Homo sapiens FKBP-associated protein (FAP48), transcript variant 2, mRNA
NM_053274	Homo sapiens FKBP-associated protein (FAP48), transcript variant 1, mRNA
NM_054113	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 3 (KIP3), mRNA
NM_003726	Homo sapiens src family associated phosphoprotein 1 (SCAP1), mRNA
NM_012308	Homo sapiens F-box and leucine-rich repeat protein 11 (FBXL11), mRNA
NM_030913	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C (SEMA6C), mRNA

NM_021163	Homo sapiens RB-associated KRAB repressor (RBAK), mRNA
NM_033632	Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila) (FBXW7), transcript variant 1, mRNA
NM_018315	Homo sapiens F-box and WD-40 domain protein 7 (archipelago homolog, Drosophila) (FBXW7), transcript variant 2, mRNA
NM_012168	Homo sapiens F-box only protein 2 (FBXO2), mRNA
NM_033332	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 3, mRNA
NM_033331	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 2, mRNA
NM_003671	Homo sapiens CDC14 cell division cycle 14 homolog B (S. cerevisiae) (CDC14B), transcript variant 1, mRNA
NM_033307	Homo sapiens caspase 4, apoptosis-related cysteine protease (CASP4), transcript variant delta, mRNA
NM_033306	Homo sapiens caspase 4, apoptosis-related cysteine protease (CASP4), transcript variant gamma, mRNA
NM_001225	Homo sapiens caspase 4, apoptosis-related cysteine protease (CASP4), transcript variant alpha, mRNA
NM_002948	Homo sapiens ribosomal protein L15 (RPL15), mRNA
NM_033228	Homo sapiens ADP-ribosylation factor domain protein 1, 64kD (ARFD1), transcript variant gamma, mRNA
NM_033227	Homo sapiens ADP-ribosylation factor domain protein 1, 64kD (ARFD1), transcript variant beta, mRNA
NM_001656	Homo sapiens ADP-ribosylation factor domain protein 1, 64kD (ARFD1), transcript variant alpha, mRNA
NM_021203	Homo sapiens APMCF1 protein (APMCF1), mRNA
NM_012095	Homo sapiens adaptor-related protein complex 3, mu 1 subunit (AP3M1), mRNA
NM_001025	Homo sapiens ribosomal protein S23 (RPS23), mRNA
NM_032989	Homo sapiens BCL2-antagonist of cell death (BAD), transcript variant 2, mRNA
NM_004322	Homo sapiens BCL2-antagonist of cell death (BAD), transcript variant 1, mRNA
NM_014326	Homo sapiens death-associated protein kinase 2 (DAPK2), mRNA
NM_012430	Homo sapiens sec22 homolog (SEC22A), mRNA
NM_031216	Homo sapiens sec13-like protein (SEC13L), mRNA
NM_002927	Homo sapiens regulator of G-protein signalling 13 (RGS13), mRNA
NM_031274	Homo sapiens testis expressed sequence 13A (TEX13A), mRNA
NM_001730	Homo sapiens Kruppel-like factor 5 (intestinal) (KLF5), mRNA
NM_032674	Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA
NM_031361	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) binding protein (COL4A3BP), transcript variant 2, mRNA
NM_031266	Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRPAB), transcript variant 1, mRNA
NM_004499	Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRPAB), transcript variant 2, mRNA
NM_004990	Homo sapiens methionine-tRNA synthetase (MARS), mRNA
NM_031244	Homo sapiens sirtuin silent mating type information regulation 2 homolog 5 (S. cerevisiae) (SIRT5), transcript variant 2, mRNA
NM_012241	Homo sapiens sirtuin silent mating type information regulation 2 homolog 5 (S. cerevisiae) (SIRT5), transcript variant 1, mRNA
NM_006845	Homo sapiens kinesin-like 6 (mitotic centromere-associated kinesin) (KNSL6), mRNA

NM_030920	Homo sapiens lecuine-rich acidic protein-like protein (LANP-L), mRNA
NM_016228	Homo sapiens L-kynurenine/alpha-aminoadipate aminotransferase (KATII), mRNA
NM_017951	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
NM_000778	Homo sapiens cytochrome P450, subfamily IVA, polypeptide 11 (CYP4A11), mRNA
NM_006582	Homo sapiens glucocorticoid modulatory element binding protein 1 (GMEB1), transcript variant 1, mRNA
NM_024482	Homo sapiens glucocorticoid modulatory element binding protein 1 (GMEB1), transcript variant 2, mRNA
NM_024885	Homo sapiens TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50 kD (TAF7L), mRNA
NM_005736	Homo sapiens ARP1 actin-related protein 1 homolog A, centractin alpha (yeast) (ACTR1A), mRNA
NM_014031	Homo sapiens VLCS-H1 protein (VLCS-H1), mRNA
NM_022334	Homo sapiens integrin cytoplasmic domain-associated protein 1 (ICAP-1A), transcript variant 2, mRNA
NM_007036	Homo sapiens endothelial cell-specific molecule 1 (ESM1), mRNA
NM_006817	Homo sapiens chromosome 12 open reading frame 8 (C12orf8), mRNA
NM_022802	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 2, mRNA
NM_001951	Homo sapiens E2F transcription factor 5, p130-binding (E2F5), mRNA
NM_022142	Homo sapiens epididymal sperm binding protein 1 (ELSPBP1), mRNA
NM_012200	Homo sapiens beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) (B3GAT3), mRNA
NM_022375	Homo sapiens oculomedin (OCLM), mRNA
NM_004962	Homo sapiens growth differentiation factor 10 (GDF10), mRNA
NM_007372	Homo sapiens RNA helicase-related protein (RNAHP), mRNA
NM_005613	Homo sapiens regulator of G-protein signalling 4 (RGS4), mRNA
NM_006083	Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA
NM_012426	Homo sapiens splicing factor 3b, subunit 3, 130kD (SF3B3), mRNA
NM_018164	Homo sapiens hypothetical protein FLJ10637 (FLJ10637), mRNA
NM_006367	Homo sapiens adenylyl cyclase-associated protein (CAP), mRNA
NM_021106	Homo sapiens regulator of G-protein signalling 3 (RGS3), mRNA
NM_021082	Homo sapiens solute carrier family 15 (H+/peptide transporter), member 2 (SLC15A2), mRNA
NM_016578	Homo sapiens HBV pX associated protein-8 (LOC51773), mRNA
NM_006671	Homo sapiens solute carrier family 1 (glutamate transporter), member 7 (SLC1A7), mRNA
NM_020650	Homo sapiens hypothetical protein LOC57333 (LOC57333), mRNA
NM_015990	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
NM_020905	Homo sapiens PAN2 protein (PAN2), mRNA
NM_020685	Homo sapiens HT021 (HT021), mRNA
NM_020682	Homo sapiens Cyt19 protein (Cyt19), mRNA
NM_020678	Homo sapiens HT017 protein (HT017), mRNA
NM_020669	Homo sapiens uncharacterized gastric protein ZA52P (LOC57399), mRNA
NM_003760	Homo sapiens eukaryotic translation initiation factor 4 gamma, 3 (EIF4G3), mRNA
NM_020412	Homo sapiens CHMP1.5 protein (CHMP1.5), mRNA
NM_020411	Homo sapiens XAGE-1 protein (XAGE-1), mRNA
NM_020408	Homo sapiens CGI-203 protein (CGI-203), mRNA
NM_020395	Homo sapiens hypothetical nuclear factor SBBI22 (LOC57117), mRNA

NM_020387	Homo sapiens CATX-8 protein (CATX-8), mRNA
NM_020371	Homo sapiens cell death regulator aven (LOC57099), mRNA
NM_020362	Homo sapiens HT014 (HT014), mRNA
NM_020307	Homo sapiens cyclin L ania-6a (LOC57018), mRNA
NM_007187	Homo sapiens WW domain binding protein 4 (formin binding protein 21) (WBP4), mRNA
NM_005644	Homo sapiens TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20 kD (TAF12), mRNA
NM_020150	Homo sapiens SAR1 protein (SAR1), mRNA
NM_020167	Homo sapiens neuromedin U receptor 2 (NMU2R), mRNA
NM_020233	Homo sapiens x 006 protein (MDS006), mRNA
NM_020232	Homo sapiens x 003 protein (MDS003), mRNA
NM_020247	Homo sapiens hypothetical protein, clone Telethon(Italy_B41)_Strait02270_FL142 (LOC56997), mRNA
NM_020213	Homo sapiens hypothetical protein from EUROIMAGE 1977056 (LOC56965), mRNA
NM_020153	Homo sapiens hypothetical protein (LOC56912), mRNA
NM_020149	Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog 2 (mouse) (MEIS2), mRNA
NM_020120	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 1 (UGCGL1), mRNA
NM_020190	Homo sapiens HNOEL-iso protein (HNOEL-iso), mRNA
NM_020242	Homo sapiens kinesin-like 7 (KNSL7), mRNA
NM_020194	Homo sapiens GL004 protein (GL004), mRNA
NM_020193	Homo sapiens GL002 protein (GL002), mRNA
NM_020189	Homo sapiens DC6 protein (DC6), mRNA
NM_020188	Homo sapiens DC13 protein (DC13), mRNA
NM_020134	Homo sapiens collapsin response mediator protein-5; CRMP3-associated molecule (CRMP5), mRNA
NM_019893	Homo sapiens mitochondrial ceramidase (ASAH2), mRNA
NM_019846	Homo sapiens CC chemokine CCL28 (SCYA28), mRNA
NM_019852	Homo sapiens putative methyltransferase (M6A), mRNA
NM_013338	Homo sapiens Alg5, S. cerevisiae, homolog of (ALG5), mRNA
NM_013341	Homo sapiens hypothetical protein (PTD004), mRNA
NM_013318	Homo sapiens hypothetical protein (LQFBS-1), mRNA
NM_013302	Homo sapiens elongation factor-2 kinase (HSU93850), mRNA
NM_013299	Homo sapiens protein predicted by clone 23627 (HSU79266), mRNA
NM_013347	Homo sapiens replication protein A complex 34 kd subunit homolog Rpa4 (HSU24186), mRNA
NM_019011	Homo sapiens TRIAD3 protein (TRIAD3), mRNA
NM_018965	Homo sapiens triggering receptor expressed on myeloid cells 2 (TREM2), mRNA
NM_019043	Homo sapiens similar to proline-rich protein 48 (LOC54518), mRNA
NM_019006	Homo sapiens protein associated with PRK1 (AWP1), mRNA
NM_019101	Homo sapiens apolipoprotein M (G3A), mRNA
NM_019049	Homo sapiens hypothetical protein (FLJ20054), mRNA
NM_018992	Homo sapiens hypothetical protein (FLJ20040), mRNA
NM_019033	Homo sapiens hypothetical protein (FLJ11235), mRNA
NM_019045	Homo sapiens similar to rab11-binding protein (FLJ11116), mRNA
NM_019079	Homo sapiens hypothetical protein (FLJ10884), mRNA
NM_019073	Homo sapiens hypothetical protein (FLJ10007), mRNA
NM_014298	Homo sapiens quinolinate phosphoribosyltransferase (nicotinate-nucleotide

	pyrophosphorylase (carboxylating)) (QPRT), mRNA
NM_012413	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
NM_018836	Homo sapiens hypothetical protein (MOT8), mRNA
NM_018643	Homo sapiens triggering receptor expressed on myeloid cells 1 (TREM1), mRNA
NM_018647	Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), mRNA
NM_018664	Homo sapiens Jun dimerization protein p21SNFT (SNFT), mRNA
NM_018540	Homo sapiens hypothetical protein PRO2831 (PRO2831), mRNA
NM_018630	Homo sapiens hypothetical protein PRO2577 (PRO2577), mRNA
NM_018527	Homo sapiens hypothetical protein PRO2435 (PRO2435), mRNA
NM_018625	Homo sapiens hypothetical protein PRO2289 (PRO2289), mRNA
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NM_018608	Homo sapiens hypothetical protein PRO1905 (PRO1905), mRNA
NM_018509	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
NM_018505	Homo sapiens hypothetical protein PRO1728 (PRO1728), mRNA
NM_018444	Homo sapiens pyruvate dehydrogenase phosphatase (PDP), mRNA
NM_018442	Homo sapiens PC326 protein (PC326), mRNA
NM_018698	Homo sapiens hypothetical protein P15-2 (P15-2), mRNA
NM_018466	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS031 (MDS031), mRNA
NM_018465	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS030 (MDS030), mRNA
NM_018463	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS028 (MDS028), mRNA
NM_018650	Homo sapiens MAP/microtubule affinity-regulating kinase 1 (MARK1), mRNA
NM_018678	Homo sapiens lipopolysaccharide specific response-68 protein (LSR68), mRNA
NM_018695	Homo sapiens erbb2 interacting protein (ERBB2IP), mRNA
NM_018683	Homo sapiens zinc finger protein 313 (ZNF313), mRNA
NM_018660	Homo sapiens papillomavirus regulatory factor PRF-1 (LOC55893), mRNA
NM_018484	Homo sapiens solute carrier family 22 (organic anion/cation transporter), member 11 (SLC22A11), mRNA
NM_018445	Homo sapiens AD-015 protein (LOC55829), mRNA
NM_017571	Homo sapiens hypothetical protein (LOC55580), mRNA
NM_017542	Homo sapiens KIAA1513 protein (KIAA1513), mRNA
NM_018473	Homo sapiens uncharacterized hypothalamus protein HT012 (HT012), mRNA
NM_018480	Homo sapiens uncharacterized hypothalamus protein HT007 (HT007), mRNA
NM_017583	Homo sapiens DIPB protein (HSA249128), mRNA
NM_017567	Homo sapiens N-acetylglucosamine kinase (NAGK), mRNA
NM_018487	Homo sapiens hepatocellular carcinoma-associated antigen 112 (HCA112), mRNA
NM_017548	Homo sapiens hypothetical protein (H41), mRNA
NM_017547	Homo sapiens hypothetical protein (H17), mRNA
NM_017966	Homo sapiens hypothetical protein FLJ20847 (FLJ20847), mRNA
NM_017955	Homo sapiens hypothetical protein FLJ20764 (FLJ20764), mRNA
NM_017948	Homo sapiens hypothetical protein FLJ20736 (FLJ20736), mRNA
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NM_017887	Homo sapiens hypothetical protein FLJ20580 (FLJ20580), mRNA
NM_017886	Homo sapiens hypothetical protein FLJ20574 (FLJ20574), mRNA
NM_017880	Homo sapiens hypothetical protein FLJ20558 (FLJ20558), mRNA
NM_017878	Homo sapiens HRAS-like suppressor 2 (HRASLS2), mRNA
NM_017877	Homo sapiens hypothetical protein FLJ20555 (FLJ20555), mRNA
NM_017875	Homo sapiens hypothetical protein FLJ20551 (FLJ20551), mRNA
NM_017870	Homo sapiens hypothetical protein FLJ20539 (FLJ20539), mRNA
NM_017867	Homo sapiens hypothetical protein FLJ20534 (FLJ20534), mRNA
NM_017864	Homo sapiens hypothetical protein FLJ20530 (FLJ20530), mRNA
NM_017857	Homo sapiens slingshot 3 (SSH-3), mRNA
NM_017852	Homo sapiens NALP2 protein (NALP2), mRNA
NM_017850	Homo sapiens hypothetical protein FLJ20508 (FLJ20508), mRNA
NM_017846	Homo sapiens tRNA selenocysteine associated protein (SECP43), mRNA
NM_017841	Homo sapiens hypothetical protein FLJ20487 (FLJ20487), mRNA
NM_017839	Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA
NM_017837	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
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NM_017810	Homo sapiens hypothetical protein FLJ20417 (FLJ20417), mRNA
NM_017802	Homo sapiens hypothetical protein FLJ20397 (FLJ20397), mRNA
NM_017792	Homo sapiens hypothetical protein FLJ20373 (FLJ20373), mRNA
NM_017790	Homo sapiens regulator of G-protein signalling 3 (RGS3), mRNA
NM_017786	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
NM_017785	Homo sapiens hypothetical protein FLJ20364 (FLJ20364), mRNA
NM_017775	Homo sapiens hypothetical protein FLJ20343 (FLJ20343), mRNA
NM_017774	Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
NM_017772	Homo sapiens hypothetical protein FLJ20337 (FLJ20337), mRNA
NM_017770	Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2), mRNA
NM_017762	Homo sapiens hypothetical protein FLJ20313 (FLJ20313), mRNA
NM_017759	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
NM_017756	Homo sapiens hypothetical protein FLJ20306 (FLJ20306), mRNA
NM_017753	Homo sapiens hypothetical protein FLJ20300 (FLJ20300), mRNA
NM_017751	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
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NM_017738	Homo sapiens hypothetical protein FLJ20276 (FLJ20276), mRNA

NM_017736	Homo sapiens hypothetical protein FLJ20274 (FLJ20274), mRNA
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NM_017719	Homo sapiens hypothetical protein FLJ20224 (FLJ20224), mRNA
NM_017718	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
NM_017716	Homo sapiens membrane-spanning 4-domains, subfamily A, member 12 4-domains, subfamily A, member 7 (MS4A12), mRNA
NM_017711	Homo sapiens hypothetical protein FLJ20207 (FLJ20207), mRNA
NM_017709	Homo sapiens hypothetical protein FLJ20202 (FLJ20202), mRNA
NM_017704	Homo sapiens hypothetical protein FLJ20189 (FLJ20189), mRNA
NM_017699	Homo sapiens hypothetical protein FLJ20174 (FLJ20174), mRNA
NM_017697	Homo sapiens hypothetical protein FLJ20171 (FLJ20171), mRNA
NM_017687	Homo sapiens hypothetical protein FLJ20147 (FLJ20147), mRNA
NM_017686	Homo sapiens ganglioside induced differentiation associated protein 2 (GDAP2), mRNA
NM_017678	Homo sapiens hypothetical protein FLJ20127 (FLJ20127), mRNA
NM_017677	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
NM_017676	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA
NM_017670	Homo sapiens hypothetical protein FLJ20113 (FLJ20113), mRNA
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NM_017665	Homo sapiens hypothetical protein FLJ20094 (FLJ20094), mRNA
NM_017659	Homo sapiens hypothetical protein FLJ20084 (FLJ20084), mRNA
NM_017657	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
NM_017645	Homo sapiens hypothetical protein FLJ20060 (FLJ20060), mRNA
NM_017640	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
NM_017637	Homo sapiens hypothetical protein FLJ20043 (FLJ20043), mRNA
NM_017636	Homo sapiens transient receptor potential cation channel, subfamily M, member 4 (TRPM4), mRNA
NM_017634	Homo sapiens hypothetical protein FLJ20038 (FLJ20038), mRNA
NM_017629	Homo sapiens hypothetical protein FLJ20033 (FLJ20033), mRNA
NM_017622	Homo sapiens hypothetical protein FLJ20014 (FLJ20014), mRNA
NM_017620	Homo sapiens hypothetical protein FLJ20011 (FLJ20011), mRNA
NM_018396	Homo sapiens putative methyltransferase (METL), mRNA
NM_018381	Homo sapiens hypothetical protein FLJ11286 (FLJ11286), mRNA
NM_018371	Homo sapiens hypothetical protein FLJ11264 (FLJ11264), mRNA
NM_018368	Homo sapiens hypothetical protein FLJ11240 (FLJ11240), mRNA
NM_018367	Homo sapiens phytoceramidase, alkaline (PHCA), mRNA
NM_018364	Homo sapiens hypothetical protein FLJ11220 (FLJ11220), mRNA
NM_018363	Homo sapiens hypothetical protein FLJ11218 (FLJ11218), mRNA
NM_018361	Homo sapiens hypothetical protein FLJ11210 (FLJ11210), mRNA
NM_018358	Homo sapiens hypothetical protein FLJ11198 (FLJ11198), mRNA
NM_018353	Homo sapiens hypothetical protein FLJ11186 (FLJ11186), mRNA
NM_018352	Homo sapiens hypothetical protein FLJ11184 (FLJ11184), mRNA
NM_018340	Homo sapiens hypothetical protein FLJ11151 (FLJ11151), mRNA
NM_018339	Homo sapiens hypothetical protein FLJ11149 (FLJ11149), mRNA
NM_018336	Homo sapiens hypothetical protein FLJ11136 (FLJ11136), mRNA
NM_018333	Homo sapiens hypothetical protein FLJ20666 (FLJ20666), mRNA
NM_018332	Homo sapiens hypothetical protein FLJ11126 (FLJ11126), mRNA
NM_018330	Homo sapiens KIAA1598 protein (KIAA1598), mRNA
NM_018322	Homo sapiens hypothetical protein FLJ11101 (FLJ11101), mRNA
NM_018318	Homo sapiens hypothetical protein FLJ11088 (FLJ11088), mRNA
NM_018310	Homo sapiens BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like (BRF2), mRNA

NM_018303	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
NM_018298	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
NM_018287	Homo sapiens hypothetical protein FLJ10971 (FLJ10971), mRNA
NM_018286	Homo sapiens hypothetical protein FLJ10970 (FLJ10970), mRNA
NM_018283	Homo sapiens hypothetical protein FLJ10956 (FLJ10956), mRNA
NM_018281	Homo sapiens hypothetical protein FLJ10948 (FLJ10948), mRNA
NM_018278	Homo sapiens hypothetical protein FLJ10933 (FLJ10933), mRNA
NM_018276	Homo sapiens slingshot 3 (SSH-3), mRNA
NM_018273	Homo sapiens hypothetical protein FLJ10922 (FLJ10922), mRNA
NM_018272	Homo sapiens hypothetical protein FLJ10921 (FLJ10921), mRNA
NM_018268	Homo sapiens hypothetical protein FLJ10904 (FLJ10904), mRNA
NM_018265	Homo sapiens hypothetical protein FLJ10901 (FLJ10901), mRNA
NM_018254	Homo sapiens hypothetical protein FLJ10876 (FLJ10876), mRNA
NM_018253	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
NM_018252	Homo sapiens hypothetical protein FLJ10874 (FLJ10874), mRNA
NM_018245	Homo sapiens hypothetical protein FLJ10851 (FLJ10851), mRNA
NM_018241	Homo sapiens hypothetical protein FLJ10846 (FLJ10846), mRNA
NM_018239	Homo sapiens hypothetical protein FLJ10751 (FLJ10751), mRNA
NM_018230	Homo sapiens nucleoporin 133kD (NUP133), mRNA
NM_018223	Homo sapiens checkpoint with forkhead and ring finger domains (CHFR), mRNA
NM_018219	Homo sapiens hypothetical protein FLJ10786 (FLJ10786), mRNA
NM_018217	Homo sapiens chromosome 20 open reading frame 31 (C20orf31), mRNA
NM_018212	Homo sapiens likely ortholog of mouse NPC derived proline rich protein 1 (FLJ10773), mRNA
NM_018211	Homo sapiens hypothetical protein FLJ10770 (KIAA1579), mRNA
NM_018207	Homo sapiens hypothetical protein FLJ10759 (FLJ10759), mRNA
NM_018205	Homo sapiens hypothetical protein FLJ10751 (FLJ10751), mRNA
NM_018192	Homo sapiens hypothetical protein FLJ10718 (FLJ10718), mRNA
NM_018188	Homo sapiens hypothetical protein FLJ10709 (FLJ10709), mRNA
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NM_018184	Homo sapiens hypothetical protein FLJ10702 (FLJ10702), mRNA
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NM_018159	Homo sapiens hypothetical protein FLJ10628 (FLJ10628), mRNA
NM_018147	Homo sapiens hypothetical protein FLJ10582 (FLJ10582), mRNA
NM_018142	Homo sapiens hypothetical protein FLJ10569 (FLJ10569), mRNA
NM_018137	Homo sapiens protein arginine N-methyltransferase 6 (PRMT6), mRNA
NM_018136	Homo sapiens hypothetical protein FLJ10517 (FLJ10517), mRNA
NM_018133	Homo sapiens hypothetical protein FLJ10546 (FLJ10546), mRNA
NM_018122	Homo sapiens hypothetical protein FLJ10514 (FLJ10514), mRNA
NM_018120	Homo sapiens hypothetical protein FLJ10511 (FLJ10511), mRNA
NM_018119	Homo sapiens hypothetical protein FLJ10509 (FLJ10509), mRNA
NM_018116	Homo sapiens misato (FLJ10504), mRNA
NM_018112	Homo sapiens hypothetical protein FLJ10493 (FLJ10493), mRNA
NM_018106	Homo sapiens hypothetical protein FLJ10479 (FLJ10479), mRNA
NM_018101	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
NM_018100	Homo sapiens hypothetical protein FLJ10466 (FLJ10466), mRNA
NM_018099	Homo sapiens hypothetical protein FLJ10462 (FLJ10462), mRNA

NM_018097	Homo sapiens hypothetical protein FLJ10460 (FLJ10460), mRNA
NM_018093	Homo sapiens hypothetical protein FLJ10439 (FLJ10439), mRNA
NM_018092	Homo sapiens hypothetical protein FLJ10430 (FLJ10430), mRNA
NM_018091	Homo sapiens hypothetical protein FLJ10422 (FLJ10422), mRNA
NM_018090	Homo sapiens hypothetical protein FLJ10420 (FLJ10420), mRNA
NM_018087	Homo sapiens hypothetical protein FLJ10407 (FLJ10407), mRNA
NM_018086	Homo sapiens fidgetin (FIGN), mRNA
NM_018078	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
NM_018076	Homo sapiens hypothetical protein FLJ10376 (FLJ10376), mRNA
NM_018075	Homo sapiens hypothetical protein FLJ10375 (FLJ10375), mRNA
NM_018072	Homo sapiens hypothetical protein FLJ10359 (FLJ10359), mRNA
NM_018070	Homo sapiens hypothetical protein FLJ10355 (FLJ10355), mRNA
NM_018060	Homo sapiens hypothetical protein FLJ10326 (FLJ10326), mRNA
NM_018054	Homo sapiens homolog of rat nadrin (RICH1), mRNA
NM_018052	Homo sapiens hypothetical protein FLJ10305 (FLJ10305), mRNA
NM_018051	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
NM_018047	Homo sapiens hypothetical protein FLJ10290 (FLJ10290), mRNA
NM_018043	Homo sapiens hypothetical protein FLJ10261 (FLJ10261), mRNA
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NM_017993	Homo sapiens hypothetical protein FLJ10094 (FLJ10094), mRNA
NM_017988	Homo sapiens hypothetical protein FLJ10074 (FLJ10074), mRNA
NM_017987	Homo sapiens Run- and FYVE-domain containing protein (Rabip4R), mRNA
NM_017976	Homo sapiens hypothetical protein FLJ10038 (FLJ10038), mRNA
NM_018409	Homo sapiens hypothetical protein DKFZp761O0113 (DKFZp761O0113), mRNA
NM_017601	Homo sapiens hypothetical protein DKFZp761H221 (DKFZp761H221), mRNA
NM_018713	Homo sapiens hypothetical protein DKFZp547M236 (DKFZp547M236), mRNA
NM_017606	Homo sapiens hypothetical protein DKFZp434K1210 (DKFZp434K1210), mRNA
NM_017546	Homo sapiens hypothetical protein (C40), mRNA
NM_018458	Homo sapiens uncharacterized bone marrow protein BM042 (BM042), mRNA
NM_018456	Homo sapiens uncharacterized bone marrow protein BM040 (BM040), mRNA
NM_018455	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
NM_018453	Homo sapiens uncharacterized bone marrow protein BM036 (BM036), mRNA
NM_018452	Homo sapiens chromosome 6 open reading frame 35 (C6orf35), mRNA
NM_018489	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
NM_004227	Homo sapiens pleckstrin homology, Sec7 and coiled/coil domains 3 (PSCD3), mRNA
NM_007014	Homo sapiens Nedd-4-like ubiquitin-protein ligase (WWP2), mRNA
NM_017431	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit

	(PRKAG3), mRNA
NM_017426	Homo sapiens nucleoporin 54kD (NUP54), mRNA
NM_016950	Homo sapiens testican 3 (HSAJ1454), mRNA
NM_017421	Homo sapiens methyltransferase COQ3 (COQ3), mRNA
NM_006854	Homo sapiens KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2 (KDELR2), mRNA
NM_015976	Homo sapiens sorting nexin 7 (SNX7), mRNA
NM_016577	Homo sapiens RAB6B, member RAS oncogene family (RAB6B), mRNA
NM_016559	Homo sapiens PXR2b protein (PXR2b), mRNA
NM_016297	Homo sapiens prenylcysteine lyase (PCL1), mRNA
NM_016524	Homo sapiens B/K protein (LOC51760), mRNA
NM_016507	Homo sapiens CDC2-related protein kinase 7 (CrkRS), mRNA
NM_016446	Homo sapiens NAG-5 protein (LOC51754), mRNA
NM_016382	Homo sapiens natural killer cell receptor 2B4 (CD244), mRNA
NM_016354	Homo sapiens solute carrier family 21 (organic anion transporter), member 12 (SLC21A12), mRNA
NM_016298	Homo sapiens muscle disease-related protein (LOC51725), mRNA
NM_016290	Homo sapiens retinoid x receptor interacting protein (LOC51720), mRNA
NM_016280	Homo sapiens carboxylesterase-related protein (LOC51716), mRNA
NM_016229	Homo sapiens cytochrome b5 reductase b5R.2 (LOC51700), mRNA
NM_016213	Homo sapiens thyroid hormone receptor interactor 4 (TRIP4), mRNA
NM_016169	Homo sapiens suppressor of fused homolog (Drosophila) (SUFU), mRNA
NM_016084	Homo sapiens RAS, dexamethasone-induced 1 (RASD1), mRNA
NM_016077	Homo sapiens CGI-147 protein (LOC51651), mRNA
NM_016023	Homo sapiens CGI-77 protein (LOC51633), mRNA
NM_016021	Homo sapiens non-canonical ubquitin conjugating enzyme 1 (NCUBE1), mRNA
NM_016003	Homo sapiens DKFZP434J154 protein (DKFZP434J154), mRNA
NM_015981	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II alpha (CAMK2A), mRNA
NM_015949	Homo sapiens CGI-20 protein (LOC51608), mRNA
NM_015881	Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA
NM_016619	Homo sapiens hypothetical protein (LOC51316), mRNA
NM_016598	Homo sapiens DHHC1 protein (LOC51304), mRNA
NM_016589	Homo sapiens M5-14 protein (LOC51300), mRNA
NM_016588	Homo sapiens neuritin (LOC51299), mRNA
NM_016582	Homo sapiens peptide transporter 3 (PHT2), mRNA
NM_016570	Homo sapiens CDA14 (LOC51290), mRNA
NM_016565	Homo sapiens E2IG2 protein (LOC51287), mRNA
NM_016561	Homo sapiens apoptosis regulator (LOC51283), mRNA
NM_016526	Homo sapiens GS15 (LOC51272), mRNA
NM_016518	Homo sapiens pipecolic acid oxidase (PIPOX), mRNA
NM_016495	Homo sapiens hypothetical protein (LOC51256), mRNA
NM_016486	Homo sapiens hypothetical protein (LOC51249), mRNA
NM_016477	Homo sapiens forkhead box P1 (FOXP1), mRNA
NM_016465	Homo sapiens hypothetical protein (LOC51238), mRNA
NM_016456	Homo sapiens hypothetical protein (LOC51235), mRNA
NM_016350	Homo sapiens ninein (GSK3B interacting protein) (NIN), mRNA
NM_016274	Homo sapiens CK2 interacting protein 1; HQ0024c protein (LOC51177), mRNA
NM_016261	Homo sapiens delta-tubulin (LOC51174), mRNA
NM_016216	Homo sapiens debranching enzyme homolog 1 (S. cerevisiae) (DBR1), mRNA
NM_016208	Homo sapiens VPS28 protein (LOC51160), mRNA
NM_016206	Homo sapiens colon carcinoma related protein (LOC51159), mRNA

NM_016185	Homo sapiens hematological and neurological expressed 1 (HN1), mRNA
NM_016181	Homo sapiens melanoma antigen (LOC51152), mRNA
NM_016139	Homo sapiens 16.7Kd protein (LOC51142), mRNA
NM_016129	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis) (COPS4), mRNA
NM_016122	Homo sapiens NY-REN-58 antigen (LOC51134), mRNA
NM_016119	Homo sapiens putative zinc finger protein NY-REN-34 antigen (LOC51131), mRNA
NM_016103	Homo sapiens GTP-binding protein Sara (LOC51128), mRNA
NM_016099	Homo sapiens HSPC041 protein (LOC51125), mRNA
NM_016096	Homo sapiens HSPC038 protein (LOC51123), mRNA
NM_016037	Homo sapiens CGI-94 protein (LOC51118), mRNA
NM_016014	Homo sapiens CGI-67 protein (LOC51104), mRNA
NM_015997	Homo sapiens CGI-41 protein (LOC51093), mRNA
NM_015974	Homo sapiens lambda-crystallin (LOC51084), mRNA
NM_015973	Homo sapiens galanin-related peptide (LOC51083), mRNA
NM_015972	Homo sapiens RNA polymerase I 16 kDa subunit (LOC51082), mRNA
NM_015953	Homo sapiens eNOS interacting protein (NOSIP), mRNA
NM_015936	Homo sapiens CGI-04 protein (LOC51067), mRNA
NM_015895	Homo sapiens geminin (LOC51053), mRNA
NM_015882	Homo sapiens RIG-like 5-6 (LOC51048), mRNA
NM_015853	Homo sapiens ORF (LOC51035), mRNA
NM_016080	Homo sapiens CGI-150 protein (LOC51031), mRNA
NM_016078	Homo sapiens CGI-148 protein (LOC51030), mRNA
NM_016076	Homo sapiens CGI-146 protein (LOC51029), mRNA
NM_016052	Homo sapiens CGI-115 protein (LOC51018), mRNA
NM_016049	Homo sapiens CGI-112 protein (LOC51016), mRNA
NM_015940	Homo sapiens CGI-10 protein (LOC51004), mRNA
NM_016505	Homo sapiens hypothetical protein (HSPC251), mRNA
NM_016485	Homo sapiens hypothetical protein (HSPC228), mRNA
NM_016472	Homo sapiens hypothetical protein (HSPC210), mRNA
NM_016464	Homo sapiens hypothetical protein (HSPC196), mRNA
NM_016462	Homo sapiens hypothetical protein (HSPC194), mRNA
NM_016535	Homo sapiens HSPC189 protein (HSPC189), mRNA
NM_016404	Homo sapiens hypothetical protein (HSPC152), mRNA
NM_016403	Homo sapiens hypothetical protein (HSPC148), mRNA
NM_016399	Homo sapiens hypothetical protein (HSPC132), mRNA
NM_016395	Homo sapiens butyrate-induced transcript 1 (HSPC121), mRNA
NM_016387	Homo sapiens hypothetical protein (HSPC060), mRNA
NM_016101	Homo sapiens hypothetical protein (HSPC031), mRNA
NM_015918	Homo sapiens homolog of yeast RNase MRP/RNase P protein Pop5 (POP5), mRNA
NM_016257	Homo sapiens hippocalcin-like protein 4 (HPCAL4), mRNA
NM_016287	Homo sapiens HP1-BP74 (HP1-BP74), mRNA
NM_015888	Homo sapiens hook1 protein (HOOK1), mRNA
NM_015852	Homo sapiens Krueppel-related zinc finger protein (H-plk), mRNA
NM_016451	Homo sapiens coatomer protein complex, subunit beta (COPB), mRNA
NM_015986	Homo sapiens cytokine receptor-like factor 3 (CRLF3), mRNA
NM_016204	Homo sapiens growth differentiation factor 2 (GDF2), mRNA
NM_016617	Homo sapiens hypothetical protein (BM-002), mRNA
NM_014822	Homo sapiens SEC24 related gene family, member D (S. cerevisiae) (SEC24D), mRNA

NM_014059	Homo sapiens RGC32 protein (RGC32), mRNA
NM_014040	Homo sapiens PTD015 protein (PTD015), mRNA
NM_014039	Homo sapiens PTD012 protein (PTD012), mRNA
NM_014111	Homo sapiens PRO2086 protein (PRO2086), mRNA
NM_014106	Homo sapiens PRO1914 protein (PRO1914), mRNA
NM_014104	Homo sapiens PRO1880 protein (PRO1880), mRNA
NM_014100	Homo sapiens PRO1770 protein (PRO1770), mRNA
NM_014137	Homo sapiens PRO0650 protein (PRO0650), mRNA
NM_014127	Homo sapiens PRO0456 protein (PRO0456), mRNA
NM_014123	Homo sapiens PRO0246 protein (PRO0246), mRNA
NM_014114	Homo sapiens PRO0097 protein (PRO0097), mRNA
NM_014113	Homo sapiens PRO0038 protein (PRO0038), mRNA
NM_014048	Homo sapiens KIAA1243 protein (KIAA1243), mRNA
NM_015368	Homo sapiens pannexin 1 (PANX1), mRNA
NM_014910	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
NM_014916	Homo sapiens KIAA1079 protein (KIAA1079), mRNA
NM_014967	Homo sapiens KIAA1018 protein (KIAA1018), mRNA
NM_014953	Homo sapiens mitotic control protein dis3 homolog (KIAA1008), mRNA
NM_014954	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
NM_014917	Homo sapiens netrin G1 (KIAA0976), mRNA
NM_014930	Homo sapiens KIAA0972 protein (KIAA0972), mRNA
NM_014907	Homo sapiens KIAA0967 protein (KIAA0967), mRNA
NM_014912	Homo sapiens KIAA0940 protein (KIAA0940), mRNA
NM_014021	Homo sapiens KIAA0923 protein (KIAA0923), mRNA
NM_014899	Homo sapiens KIAA0878 protein (KIAA0878), mRNA
NM_014951	Homo sapiens KIAA0844 protein (KIAA0844), mRNA
NM_014729	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
NM_014813	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
NM_014829	Homo sapiens RNA helicase (KIAA0801), mRNA
NM_014698	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
NM_014824	Homo sapiens KIAA0769 gene product (KIAA0769), mRNA
NM_014677	Homo sapiens KIAA0751 gene product (KIAA0751), mRNA
NM_014705	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
NM_014861	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
NM_014721	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
NM_014827	Homo sapiens KIAA0663 gene product (KIAA0663), mRNA
NM_014645	Homo sapiens KIAA0635 gene product (KIAA0635), mRNA
NM_014664	Homo sapiens KIAA0615 gene product (KIAA0615), mRNA
NM_014834	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
NM_014696	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
NM_014732	Homo sapiens KIAA0513 gene product (KIAA0513), mRNA
NM_014710	Homo sapiens KIAA0443 gene product (KIAA0443), mRNA
NM_014797	Homo sapiens KIAA0441 gene product (KIAA0441), mRNA
NM_014819	Homo sapiens KIAA0438 gene product (KIAA0438), mRNA
NM_015216	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
NM_015251	Homo sapiens KIAA0431 protein (KIAA0431), mRNA
NM_015185	Homo sapiens Cdc42 guanine nucleotide exchange factor (GEF) 9 (ARHGEF9), mRNA
NM_014711	Homo sapiens KIAA0419 gene product (KIAA0419), mRNA
NM_015564	Homo sapiens KIAA0416 protein (KIAA0416), mRNA
NM_014778	Homo sapiens KIAA0410 gene product (KIAA0410), mRNA

NM_014659	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
NM_014639	Homo sapiens KIAA0372 gene product (KIAA0372), mRNA
NM_014786	Homo sapiens KIAA0337 gene product (KIAA0337), mRNA
NM_014845	Homo sapiens KIAA0274 gene product (KIAA0274), mRNA
NM_014745	Homo sapiens KIAA0233 gene product (KIAA0233), mRNA
NM_014643	Homo sapiens KIAA0222 gene product (KIAA0222), mRNA
NM_014674	Homo sapiens KIAA0212 gene product (KIAA0212), mRNA
NM_014720	Homo sapiens Ste20-related serine/threonine kinase (SLK), mRNA
NM_014761	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
NM_014730	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
NM_014661	Homo sapiens KIAA0140 gene product (KIAA0140), mRNA
NM_014777	Homo sapiens KIAA0133 gene product (KIAA0133), mRNA
NM_014815	Homo sapiens KIAA0130 gene product (KIAA0130), mRNA
NM_014755	Homo sapiens transcriptional regulator interacting with the PHS-bromodomain 2 (TRIP-Br2), mRNA
NM_014628	Homo sapiens gene predicted from cDNA with a complete coding sequence (KIAA0110), mRNA
NM_014814	Homo sapiens KIAA0107 gene product (KIAA0107), mRNA
NM_014752	Homo sapiens KIAA0102 gene product (KIAA0102), mRNA
NM_014780	Homo sapiens KIAA0076 gene product (KIAA0076), mRNA
NM_014882	Homo sapiens KIAA0053 gene product (KIAA0053), mRNA
NM_014750	Homo sapiens KIAA0008 gene product (KIAA0008), mRNA
NM_015684	Homo sapiens mitochondrial ATP synthase regulatory component factor B (ATPW), mRNA
NM_014186	Homo sapiens HSPC166 protein (HSPC166), mRNA
NM_014184	Homo sapiens HSPC163 protein (HSPC163), mRNA
NM_014181	Homo sapiens HSPC159 protein (HSPC159), mRNA
NM_014179	Homo sapiens HSPC157 protein (HSPC157), mRNA
NM_014166	Homo sapiens HSPC126 protein (HSPC126), mRNA
NM_014155	Homo sapiens HSPC063 protein (HSPC063), mRNA
NM_014038	Homo sapiens HSPC028 protein (HSPC028), mRNA
NM_014017	Homo sapiens HSPC003 protein (HSPC003), mRNA
NM_014053	Homo sapiens FLVCR protein (FLVCR), mRNA
NM_015400	Homo sapiens DKFZP586N0721 protein (DKFZP586N0721), mRNA
NM_015583	Homo sapiens DKFZP586M0622 protein (DKFZP586M0622), mRNA
NM_015485	Homo sapiens DKFZP566K023 protein (DKFZP566K023), mRNA
NM_014043	Homo sapiens DKFZP564O123 protein (DKFZP564O123), mRNA
NM_015387	Homo sapiens preimplantation protein 3 (PREI3), mRNA
NM_014056	Homo sapiens DKFZP564K247 protein (DKFZP564K247), mRNA
NM_015623	Homo sapiens putative ankyrin-repeat containing protein (DKFZP564D166), mRNA
NM_015582	Homo sapiens DKFZP564B147 protein (DKFZP564B147), mRNA
NM_015610	Homo sapiens DKFZP434J154 protein (DKFZP434J154), mRNA
NM_015590	Homo sapiens DKFZP434F1735 protein (DKFZP434F1735), mRNA
NM_015644	Homo sapiens DKFZP434B103 protein (DKFZP434B103), mRNA
NM_015396	Homo sapiens DKFZP434A043 protein (DKFZP434A043), mRNA
NM_014058	Homo sapiens DESC1 protein (DESC1), mRNA
NM_015680	Homo sapiens hypothetical protein (CGI-57), mRNA
NM_015379	Homo sapiens brain protein I3 (BRI3), mRNA
NM_014580	Homo sapiens solute carrier family 2, (facilitated glucose transporter) member 8 (SLC2A8), mRNA
NM_014280	Homo sapiens DnaJ (Hsp40) homolog, subfamily C, member 8 (DNAJC8),

	mRNA
NM_014313	Homo sapiens small membrane protein 1 (SMP1), mRNA
NM_014229	Homo sapiens solute carrier family 6 (neurotransmitter transporter, GABA), member 11 (SLC6A11), mRNA
NM_014575	Homo sapiens schwannomin interacting protein 1 (SCHIP1), mRNA
NM_014402	Homo sapiens low molecular mass ubiquinone-binding protein (9.5kD) (QP-C), mRNA
NM_014394	Homo sapiens growth hormone inducible transmembrane protein (GHITM), mRNA
NM_014225	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA
NM_014497	Homo sapiens nuclear protein (NP220), mRNA
NM_014399	Homo sapiens tetraspan NET-6 protein (NET-6), mRNA
NM_014889	Homo sapiens metalloprotease 1 (pitrilysin family) (MP1), mRNA
NM_014484	Homo sapiens molybdenum cofactor synthesis 3 (MOCS3), mRNA
NM_014447	Homo sapiens arfaptin 1 (HSU52521), mRNA
NM_014350	Homo sapiens TNF-induced protein (GG2-1), mRNA
NM_014478	Homo sapiens calcitonin gene-related peptide-receptor component protein (CGRP-RCP), mRNA
NM_014482	Homo sapiens bone morphogenetic protein 10 (BMP10), mRNA
NM_014474	Homo sapiens acid sphingomyelinase-like phosphodiesterase (ASML3B), mRNA
NM_014480	Homo sapiens zinc finger protein (AF020591), mRNA
NM_014576	Homo sapiens Apobec-1 complementation factor; APOBEC-1 stimulating protein (ACF), mRNA
NM_005884	Homo sapiens p21(CDKN1A)-activated kinase 4 (PAK4), mRNA
NM_013434	Homo sapiens calsenilin, presenilin binding protein, EF hand transcription factor (CSEN), mRNA
NM_012446	Homo sapiens single-stranded DNA binding protein 2 (SSBP2), mRNA
NM_013235	Homo sapiens putative ribonuclease III (RNASE3L), mRNA
NM_013349	Homo sapiens secreted protein of unknown function (SPUF), mRNA
NM_013323	Homo sapiens sorting nexin 11 (SNX11), mRNA
NM_013388	Homo sapiens prolactin regulatory element binding (PREB), mRNA
NM_013328	Homo sapiens pyrroline 5-carboxylate reductase isoform (P5CR2), mRNA
NM_013370	Homo sapiens pregnancy-induced growth inhibitor (OKL38), mRNA
NM_013277	Homo sapiens Rac GTPase activating protein 1 (RACGAP1), mRNA
NM_013285	Homo sapiens nucleolar GTPase (HUMAUANTIG), mRNA
NM_013320	Homo sapiens host cell factor 2 (HCF-2), mRNA
NM_013391	Homo sapiens dimethylglycine dehydrogenase precursor (DMGDH), mRNA
NM_013253	Homo sapiens dickkopf homolog 3 (Xenopus laevis) (DKK3), mRNA
NM_013339	Homo sapiens dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase (ALG6), mRNA
NM_004120	Homo sapiens guanylate binding protein 2, interferon-inducible (GBP2), mRNA
NM_005690	Homo sapiens dynamin 1-like (DNM1L), transcript variant 3, mRNA
NM_012063	Homo sapiens dynamin 1-like (DNM1L), transcript variant 2, mRNA
NM_012470	Homo sapiens transportin-SR (TRN-SR), mRNA
NM_012252	Homo sapiens transcription factor EC (TFEC), mRNA
NM_012250	Homo sapiens related RAS viral (r-ras) oncogene homolog 2 (RRAS2), mRNA
NM_012249	Homo sapiens ras-like protein (TC10), mRNA
NM_012388	Homo sapiens pallidin homolog (mouse) (PLDN), mRNA
NM_012322	Homo sapiens U6 snRNA-associated Sm-like protein (LSM5), mRNA
NM_012316	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA

NM_012189	Homo sapiens fibrousheathin II (FSP-2), mRNA
NM_012081	Homo sapiens ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR (ELL2), mRNA
NM_003996	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
NM_005260	Homo sapiens growth differentiation factor 9 (GDF9), mRNA
NM_007352	Homo sapiens elastase 3B, pancreatic (ELA3B), mRNA
NM_006685	Homo sapiens proline rich 3 (PROL3), mRNA
NM_007357	Homo sapiens low density lipoprotein receptor defect C complementing (LDLC), mRNA
NM_004133	Homo sapiens hepatocyte nuclear factor 4, gamma (HNF4G), mRNA
NM_003144	Homo sapiens signal sequence receptor, alpha (translocon-associated protein alpha) (SSR1), mRNA
NM_007324	Homo sapiens MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 1, mRNA
NM_007323	Homo sapiens MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 2, mRNA
NM_005162	Homo sapiens angiotensin receptor-like 2 (AGTRL2), mRNA
NM_005501	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant b, mRNA
NM_007144	Homo sapiens zinc finger protein 144 (Mel-18) (ZNF144), mRNA
NM_007286	Homo sapiens synaptopodin (KIAA1029), mRNA
NM_007199	Homo sapiens interleukin-1 receptor-associated kinase M (IRAK-M), mRNA
NM_007283	Homo sapiens monoglyceride lipase (MGLL), mRNA
NM_007241	Homo sapiens EAP30 subunit of ELL complex (EAP30), mRNA
NM_007212	Homo sapiens ring finger protein 2 (RNF2), mRNA
NM_007236	Homo sapiens calcium binding protein P22 (CHP), mRNA
NM_007063	Homo sapiens vascular Rab-GAP/TBC-containing (VRP), mRNA
NM_007027	Homo sapiens topoisomerase (DNA) II binding protein (TOPBP1), mRNA
NM_006938	Homo sapiens small nuclear ribonucleoprotein D1 polypeptide (16kD) (SNRPD1), mRNA
NM_006937	Homo sapiens SMT3 suppressor of mif two 3 homolog 2 (yeast) (SMT3H2), mRNA
NM_007029	Homo sapiens stathmin-like 2 (STMN2), mRNA
NM_007042	Homo sapiens ribonuclease P (14kD) (RPP14), mRNA
NM_006907	Homo sapiens pyrroline-5-carboxylate reductase 1 (PYCR1), nuclear gene encoding mitochondrial protein, mRNA
NM_007059	Homo sapiens kaptin (actin binding protein) (KPTN), mRNA
NM_007069	Homo sapiens HRAS-like suppressor 3 (HRASLS3), mRNA
NM_006895	Homo sapiens histamine N-methyltransferase (HNMT), mRNA
NM_007071	Homo sapiens HERV-H LTR-associating 3 (HHLA3), mRNA
NM_007067	Homo sapiens histone acetyltransferase (HBOA), mRNA
NM_007006	Homo sapiens cleavage and polyadenylation specific factor 5, 25 kD subunit (CPSF5), mRNA
NM_007053	Homo sapiens natural killer cell receptor, immunoglobulin superfamily member (BY55), mRNA
NM_006754	Homo sapiens synaptophysin-like protein (SYPL), mRNA
NM_006802	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
NM_006842	Homo sapiens splicing factor 3b, subunit 2, 145kD (SF3B2), mRNA
NM_006834	Homo sapiens RAB32, member RAS oncogene family (RAB32), mRNA

NM_006875	Homo sapiens pim-2 oncogene (PIM2), mRNA
NM_006810	Homo sapiens for protein disulfide isomerase-related (PDIR), mRNA
NM_003609	Homo sapiens HIRA interacting protein 3 (HIRIP3), mRNA
NM_006820	Homo sapiens chromosome 1 open reading frame 29 (C1orf29), mRNA
NM_006848	Homo sapiens hepatitis delta antigen-interacting protein A (DIPA), mRNA
NM_006876	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (B3GNT6), mRNA
NM_006653	Homo sapiens suc1-associated neurotrophic factor target 2 (FGFR signalling adaptor) (SNT-2), mRNA
NM_006638	Homo sapiens ribonuclease P, 40kD subunit (RPP40), mRNA
NM_004163	Homo sapiens RAB27B, member RAS oncogene family (RAB27B), mRNA
NM_006713	Homo sapiens activated RNA polymerase II transcription cofactor 4 (PC4), mRNA
NM_006601	Homo sapiens unactive progesterone receptor, 23 kD (P23), mRNA
NM_006675	Homo sapiens tetraspan transmembrane 4 super family (NET-5), mRNA
NM_006501	Homo sapiens myelin-associated oligodendrocyte basic protein (MOBP), mRNA
NM_006612	Homo sapiens kinesin family member 1C (KIF1C), mRNA
NM_006567	Homo sapiens phenylalanine-tRNA synthetase (FARS1), nuclear gene encoding mitochondrial protein, mRNA
NM_006594	Homo sapiens adaptor-related protein complex 4, beta 1 subunit (AP4B1), mRNA
NM_006621	Homo sapiens S-adenosylhomocysteine hydrolase-like 1 (AHCYL1), mRNA
NM_006472	Homo sapiens thioredoxin interacting protein (TXNIP), mRNA
NM_006388	Homo sapiens HIV-1 Tat interactive protein, 60 kD (HTATIP), mRNA
NM_006281	Homo sapiens serine/threonine kinase 3 (STE20 homolog, yeast) (STK3), mRNA
NM_006401	Homo sapiens acidic protein rich in leucines (SSP29), mRNA
NM_006425	Homo sapiens step II splicing factor SLU7 (SLU7), mRNA
NM_006359	Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), isoform 6 (SLC9A6), mRNA
NM_006328	Homo sapiens RNA binding motif protein 14 (RBM14), mRNA
NM_006466	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide F (39 kD) (POLR3F), mRNA
NM_006467	Homo sapiens polymerase (RNA) III (DNA directed) (32kD) (RPC32), mRNA
NM_006397	Homo sapiens ribonuclease HI, large subunit (RNASEHI), mRNA
NM_006443	Homo sapiens putative c-Myc-responsive (RCL), mRNA
NM_006390	Homo sapiens RAN binding protein 8 (RANBP8), mRNA
NM_006256	Homo sapiens protein kinase C-like 2 (PRKCL2), mRNA
NM_006254	Homo sapiens protein kinase C, delta (PRKCD), mRNA
NM_006229	Homo sapiens pancreatic lipase-related protein 1 (PNLIPRP1), mRNA
NM_006319	Homo sapiens CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) (CDIPT), mRNA
NM_006219	Homo sapiens phosphoinositide-3-kinase, catalytic, beta polypeptide (PIK3CB), mRNA
NM_006346	Homo sapiens progesterone-induced blocking factor 1 (PIBF1), mRNA
NM_006473	Homo sapiens TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kD (TAF6L), mRNA
NM_006396	Homo sapiens Sjogren's syndrome/scleroderma autoantigen 1 (SSSCA1), mRNA
NM_006428	Homo sapiens melanoma-associated antigen recognised by cytotoxic T lymphocytes (MAAT1), mRNA
NM_006475	Homo sapiens osteoblast specific factor 2 (fasciclin I-like) (OSF-2), mRNA
NM_006392	Homo sapiens nucleolar protein 5A (56kD with KKE/D repeat) (NOL5A),

	mRNA
NM_006417	Homo sapiens interferon-induced, hepatitis C-associated microtubular aggregate protein (44kD) (MTAP44), mRNA
NM_006405	Homo sapiens transmembrane 9 superfamily member 1 (TM9SF1), mRNA
NM_006471	Homo sapiens myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA
NM_006152	Homo sapiens lymphoid-restricted membrane protein (LRMP), mRNA
NM_006460	Homo sapiens HMBA-inducible (HIS1), mRNA
NM_006365	Homo sapiens transcriptional activator of the c-fos promoter (CROC4), mRNA
NM_006135	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1 (CAPZA1), mRNA
NM_006086	Homo sapiens tubulin, beta, 4 (TUBB4), mRNA
NM_005761	Homo sapiens plexin C1 (PLXNC1), mRNA
NM_005724	Homo sapiens tetraspan 3 (TSPAN-3), mRNA
NM_005646	Homo sapiens TAR (HIV) RNA binding protein 1 (TARBP1), mRNA
NM_005819	Homo sapiens syntaxin 6 (STX6), mRNA
NM_005866	Homo sapiens sigma receptor (SR31747 binding protein 1) (SR-BP1), mRNA
NM_005842	Homo sapiens sprouty homolog 2 (Drosophila) (SPRY2), mRNA
NM_005626	Homo sapiens splicing factor, arginine/serine-rich 4 (SFRS4), mRNA
NM_005770	Homo sapiens small EDRK-rich factor 2 (SERF2), mRNA
NM_005805	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
NM_005746	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
NM_005869	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
NM_005787	Homo sapiens Not56 (D. melanogaster)-like protein (NOT56L), mRNA
NM_005792	Homo sapiens M-phase phosphoprotein 6 (MPHOSPH6), mRNA
NM_005693	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
NM_005799	Homo sapiens PDZ domain protein (Drosophila inaD-like) (INADL), mRNA
NM_005713	Homo sapiens collagen, type IV, alpha 3 (Goodpasture antigen) binding protein (COL4A3BP), transcript variant 1, mRNA
NM_005878	Homo sapiens trinucleotide repeat containing 3 (TNRC3), mRNA
NM_005875	Homo sapiens translation factor sui1 homolog (GC20), mRNA
NM_005838	Homo sapiens glycine-N-acyltransferase (GLYAT), nuclear gene encoding mitochondrial protein, mRNA
NM_005754	Homo sapiens Ras-GTPase-activating protein SH3-domain-binding protein (G3BP), mRNA
NM_005764	Homo sapiens epithelial protein up-regulated in carcinoma, membrane associated protein 17 (DD96), mRNA
NM_005694	Homo sapiens COX17 homolog, cytochrome c oxidase assembly protein (yeast) (COX17), nuclear gene encoding mitochondrial protein, mRNA
NM_005506	Homo sapiens CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2 (lysosomal integral membrane protein II) (CD36L2), mRNA
NM_005881	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase (BCKDK), mRNA
NM_005718	Homo sapiens actin related protein 2/3 complex, subunit 4 (20 kD) (ARPC4), mRNA
NM_005717	Homo sapiens actin related protein 2/3 complex, subunit 5 (16 kD) (ARPC5), mRNA
NM_005829	Homo sapiens adaptor-related protein complex 3, sigma 2 subunit (AP3S2), mRNA
NM_005814	Homo sapiens glycoprotein A33 (transmembrane) (GPA33), mRNA

NM_005406	Homo sapiens Rho-associated, coiled-coil containing protein kinase 1 (ROCK1), mRNA
NM_005399	Homo sapiens protein kinase, AMP-activated, beta 2 non-catalytic subunit (PRKAB2), mRNA
NM_005396	Homo sapiens pancreatic lipase-related protein 2 (PNLIPRP2), mRNA
NM_005489	Homo sapiens SH2 domain-containing 3C (SH2D3C), mRNA
NM_005479	Homo sapiens frequently rearranged in advanced T-cell lymphomas (FRAT1), mRNA
NM_005154	Homo sapiens ubiquitin specific protease 8 (USP8), mRNA
NM_005066	Homo sapiens splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) (SFPQ), mRNA
NM_005123	Homo sapiens nuclear receptor subfamily 1, group H, member 4 (NR1H4), mRNA
NM_005046	Homo sapiens kallikrein 7 (chymotryptic, stratum corneum) (KLK7), mRNA
NM_005030	Homo sapiens polo-like kinase (Drosophila) (PLK), mRNA
NM_005014	Homo sapiens osteomodulin (OMD), mRNA
NM_005003	Homo sapiens NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1 (8kD, SDAP) (NDUFAB1), mRNA
NM_004941	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase) (DDX8), mRNA
NM_004205	Homo sapiens ubiquitin specific protease 2 (USP2), mRNA
NM_004818	Homo sapiens prp28, U5 snRNP 100 kd protein (U5-100K), mRNA
NM_004275	Homo sapiens TRF-proximal protein (TRFP), mRNA
NM_004272	Homo sapiens Homer, neuronal immediate early gene, 1B (SYN47), mRNA
NM_004177	Homo sapiens syntaxin 3A (STX3A), mRNA
NM_004719	Homo sapiens splicing factor, arginine/serine-rich 2, interacting protein (SFRS2IP), mRNA
NM_004175	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3), mRNA
NM_004592	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila) (SFRS8), mRNA
NM_004799	Homo sapiens MAD, mothers against decapentaplegic homolog (Drosophila) interacting protein, receptor activation anchor (MADHIP), transcript variant 3, mRNA
NM_004875	Homo sapiens RNA polymerase I subunit (RPA40), mRNA
NM_004292	Homo sapiens ras inhibitor (RIN1), mRNA
NM_004815	Homo sapiens PTPL1-associated RhoGAP 1 (PARG1), mRNA
NM_004772	Homo sapiens P311 protein (P311), mRNA
NM_004553	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme Q reductase) (NDUFS6), mRNA
NM_004549	Homo sapiens NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, B14.5b) (NDUFC2), mRNA
NM_004271	Homo sapiens MD-1, RP105-associated (MD-1), mRNA
NM_004672	Homo sapiens mitogen-activated protein kinase kinase kinase 6 (MAP3K6), mRNA
NM_004828	Homo sapiens lymphocyte antigen 95 (activating NK-receptor; NK-p44) (LY95), mRNA
NM_004735	Homo sapiens leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1), mRNA
NM_004811	Homo sapiens leupaxin (LPXN), mRNA
NM_004522	Homo sapiens kinesin family member 5C (KIF5C), mRNA
NM_004905	Homo sapiens anti-oxidant protein 2 (non-selenium glutathione peroxidase,

	acidic calcium-independent phospholipase A2) (KIAA0106), mRNA
NM_004770	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 2 (KCNB2), mRNA
NM_004848	Homo sapiens basement membrane-induced gene (ICB-1), mRNA
NM_004763	Homo sapiens integrin cytoplasmic domain-associated protein 1 (ICAP-1A), transcript variant 1, mRNA
NM_004814	Homo sapiens U5 snRNP-specific 40 kDa protein (hPrp8-binding) (HPRP8BP), mRNA
NM_004839	Homo sapiens Homer, neuronal immediate early gene, 2 (HOMER-2B), mRNA
NM_004684	Homo sapiens SPARC-like 1 (mast9, hevin) (SPARCL1), mRNA
NM_004832	Homo sapiens glutathione-S-transferase like; glutathione transferase omega (GSTTLp28), mRNA
NM_004486	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2), mRNA
NM_004125	Homo sapiens guanine nucleotide binding protein 10 (GNG10), mRNA
NM_004483	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH), mRNA
NM_004767	Homo sapiens endothelin type b receptor-like protein 2 (ET(B)R-LP-2), mRNA
NM_004440	Homo sapiens EphA7 (EPHA7), mRNA
NM_004757	Homo sapiens small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating) (SCYE1), mRNA
NM_004427	Homo sapiens early development regulator 2 (polyhomeotic 2 homolog) (EDR2), mRNA
NM_004422	Homo sapiens dishevelled, dsh homolog 2 (Drosophila) (DVL2), mRNA
NM_004416	Homo sapiens deltex homolog 1 (Drosophila) (DTX1), mRNA
NM_004073	Homo sapiens cytokine-inducible kinase (CNK), mRNA
NM_004365	Homo sapiens centrin, EF-hand protein, 3 (CDC31 homolog, yeast) (CETN3), mRNA
NM_004680	Homo sapiens chromodomain protein, Y chromosome, 1 (CDY1), mRNA
NM_004291	Homo sapiens cocaine- and amphetamine-regulated transcript (CART), mRNA
NM_004330	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 2 (BNIP2), mRNA
NM_004024	Homo sapiens activating transcription factor 3 (ATF3), mRNA
NM_001177	Homo sapiens ADP-ribosylation factor-like 1 (ARL1), mRNA
NM_001545	Homo sapiens immature colon carcinoma transcript 1 (ICT1), mRNA
NM_001533	Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRPL), mRNA
NM_001509	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 1, mRNA
NM_001349	Homo sapiens aspartyl-tRNA synthetase (DARS), mRNA
NM_001329	Homo sapiens C-terminal binding protein 2 (CTBP2), transcript variant 1, mRNA
NM_000082	Homo sapiens Cockayne syndrome 1 (classical) (CKN1), mRNA
NM_001277	Homo sapiens choline kinase (CHK), mRNA
NM_001087	Homo sapiens angio-associated, migratory cell protein (AAMP), mRNA
NM_003999	Homo sapiens oncostatin M receptor (OSMR), mRNA
NM_003904	Homo sapiens zinc finger protein 259 (ZNF259), mRNA
NM_003385	Homo sapiens visinin-like 1 (VSNL1), mRNA
NM_003348	Homo sapiens ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast) (UBE2N), mRNA
NM_003341	Homo sapiens ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast) (UBE2E1), mRNA
NM_003339	Homo sapiens ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast) (UBE2D2), mRNA

NM_003115	Homo sapiens UDP-N-acteylglucosamine pyrophosphorylase 1 (UAP1), mRNA
NM_003305	Homo sapiens transient receptor potential cation channel, subfamily C, member 3 (TRPC3), mRNA
NM_003596	Homo sapiens tyrosylprotein sulfotransferase 1 (TPST1), mRNA
NM_003747	Homo sapiens tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase (TNKS), mRNA
NM_003569	Homo sapiens syntaxin 7 (STX7), mRNA
NM_003164	Homo sapiens syntaxin 5A (STX5A), mRNA
NM_003764	Homo sapiens syntaxin 11 (STX11), mRNA
NM_003133	Homo sapiens signal recognition particle 9kD (SRP9), mRNA
NM_003136	Homo sapiens signal recognition particle 54kD (SRP54), mRNA
NM_003131	Homo sapiens serum response factor (c-fos serum response element-binding transcription factor) (SRF), mRNA
NM_003795	Homo sapiens sorting nexin 3 (SNX3), mRNA
NM_003096	Homo sapiens small nuclear ribonucleoprotein polypeptide G (SNRPG), mRNA
NM_003093	Homo sapiens small nuclear ribonucleoprotein polypeptide C (SNRPC), mRNA
NM_003080	Homo sapiens sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase) (SMPD2), mRNA
NM_003059	Homo sapiens solute carrier family 22 (organic cation transporter), member 4 (SLC22A4), mRNA
NM_003033	Homo sapiens sialyltransferase 4A (beta-galactosidase alpha-2,3-sialytransferase) (SIAT4A), mRNA
NM_003952	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 2 (RPS6KB2), mRNA
NM_003729	Homo sapiens RTC domain containing 1 (RTCD1), mRNA
NM_002937	Homo sapiens ribonuclease, RNase A family, 4 (RNASE4), mRNA
NM_003804	Homo sapiens receptor (TNFRSF)-interacting serine-threonine kinase 1 (RIPK1), mRNA
NM_002898	Homo sapiens RNA binding motif, single stranded interacting protein 2 (RBMS2), mRNA
NM_002886	Homo sapiens RAP2B, member of RAS oncogene family (RAP2B), mRNA
NM_003953	Homo sapiens myelin protein zero-like 1 (MPZL1), mRNA
NM_002809	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), mRNA
NM_002771	Homo sapiens protease, serine, 3 (trypsin 3) (PRSS3), mRNA
NM_002757	Homo sapiens mitogen-activated protein kinase kinase 5 (MAP2K5), mRNA
NM_002754	Homo sapiens mitogen-activated protein kinase 13 (MAPK13), mRNA
NM_003668	Homo sapiens mitogen-activated protein kinase-activated protein kinase 5 (MAPKAPK5), mRNA
NM_002718	Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), beta isoform (PPP2R3), mRNA
NM_003622	Homo sapiens PTPRF interacting protein, binding protein 1 (liprin beta 1) (PPFIBP1), mRNA
NM_003626	Homo sapiens protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1 (PPFIA1), mRNA
NM_002689	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
NM_002685	Homo sapiens polymyositis/scleroderma autoantigen 2 (100kD) (PMSCL2), mRNA
NM_003876	Homo sapiens putative receptor protein (PMI), mRNA
NM_002670	Homo sapiens plastin 1 (I isoform) (PLS1), mRNA
NM_002664	Homo sapiens pleckstrin (PLEK), mRNA
NM_003559	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta

	(PIP5K2B), mRNA
NM_003629	Homo sapiens phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma) (PIK3R3), mRNA
NM_002649	Homo sapiens phosphoinositide-3-kinase, catalytic, gamma polypeptide (PIK3CG), mRNA
NM_002624	Homo sapiens prefoldin 5 (PFDN5), mRNA
NM_003846	Homo sapiens peroxisomal biogenesis factor 11B (PEX11B), mRNA
NM_002617	Homo sapiens peroxisome biogenesis factor 10 (PEX10), mRNA
NM_002611	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 2 (PDK2), mRNA
NM_000923	Homo sapiens phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila) (PDE4C), mRNA
NM_002599	Homo sapiens phosphodiesterase 2A, cGMP-stimulated (PDE2A), mRNA
NM_002504	Homo sapiens nuclear transcription factor, X-box binding 1 (NFX1), mRNA
NM_002482	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP), mRNA
NM_003826	Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, gamma (NAPG), mRNA
NM_002465	Homo sapiens myosin binding protein C, slow type (MYBPC1), mRNA
NM_002461	Homo sapiens mevalonate (diphospho) decarboxylase (MVD), mRNA
NM_003676	Homo sapiens degenerative spermatocyte homolog, lipid desaturase (Drosophila) (DEGS), mRNA
NM_002307	Homo sapiens lectin, galactoside-binding, soluble, 7 (galectin 7) (LGALS7), mRNA
NM_002271	Homo sapiens karyopherin (importin) beta 3 (KPNB3), mRNA
NM_002270	Homo sapiens karyopherin (importin) beta 2 (KPNB2), mRNA
NM_002214	Homo sapiens integrin, beta 8 (ITGB8), mRNA
NM_002204	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), transcript variant a, mRNA
NM_001560	Homo sapiens interleukin 13 receptor, alpha 1 (IL13RA1), mRNA
NM_002163	Homo sapiens interferon consensus sequence binding protein 1 (ICSBP1), mRNA
NM_002156	Homo sapiens heat shock 60kD protein 1 (chaperonin) (HSPD1), mRNA
NM_002149	Homo sapiens hippocalcin-like 1 (HPCAL1), mRNA
NM_003947	Homo sapiens huntingtin-associated protein interacting protein (duo) (HAPIP), mRNA
NM_003665	Homo sapiens ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) (FCN3), mRNA
NM_000842	Homo sapiens glutamate receptor, metabotropic 5 (GRM5), mRNA
NM_002053	Homo sapiens guanylate binding protein 1, interferon-inducible, 67kD (GBP1), mRNA
NM_001482	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM), mRNA
NM_002044	Homo sapiens galactokinase 2 (GALK2), mRNA
NM_001417	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
NM_003758	Homo sapiens eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD) (EIF3S1), mRNA
NM_001404	Homo sapiens eukaryotic translation elongation factor 1 gamma (EEF1G), mRNA
NM_001960	Homo sapiens eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), mRNA
NM_003792	Homo sapiens endothelial differentiation-related factor 1 (EDF1), mRNA
NM_003974	Homo sapiens docking protein 2, 56kD (DOK2), mRNA

NM_003586	Homo sapiens double C2-like domains, alpha (DOC2A), mRNA
NM_001883	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2), mRNA
NM_001873	Homo sapiens carboxypeptidase E (CPE), mRNA
NM_001782	Homo sapiens CD72 antigen (CD72), mRNA
NM_001762	Homo sapiens chaperonin containing TCP1, subunit 6A (zeta 1) (CCT6A), mRNA
NM_003716	Homo sapiens Ca2+-dependent activator protein for secretion (CADPS), mRNA
NM_003986	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1 (BBOX1), mRNA
NM_001674	Homo sapiens activating transcription factor 3 (ATF3), mRNA
NM_001173	Homo sapiens Rho GTPase activating protein 5 (ARHGAP5), mRNA
NM_025065	Homo sapiens RNA processing factor 1 (RPF1), mRNA
NM_024907	Homo sapiens F-box protein FBG4 (FBG4), mRNA
NM_025194	Homo sapiens inositol 1,4,5-trisphosphate 3-kinase C (ITPKC), mRNA
NM_014203	Homo sapiens adaptor-related protein complex 2, alpha 1 subunit (AP2A1), mRNA
NM_130786	Homo sapiens alpha-1-B glycoprotein (A1BG), mRNA
NM_031482	Homo sapiens hypothetical protein DKFZp586I0418 (DKFZP586I0418), mRNA
NM_015419	Homo sapiens adlican (DKFZp564I1922), mRNA
NM_015683	Homo sapiens hypothetical protein (CLONE24945), mRNA
NM_015638	Homo sapiens chromosome 20 open reading frame 188 (C20orf188), mRNA
NM_080737	Homo sapiens synaptotagmin-like 4 (granuphilin-a) (SYTL4), mRNA
NM_080723	Homo sapiens vesicular membrane protein p24 (VMP), mRNA
NM_080678	Homo sapiens NEDD8-conjugating enzyme (NCE2), mRNA
NM_080668	Homo sapiens similar to RIKEN cDNA 2610036L13 (MGC16386), mRNA
NM_080666	Homo sapiens similar to RIKEN cDNA 2600001A11 gene (LOC112840), mRNA
NM_080663	Homo sapiens similar to RIKEN cDNA 4933424N09 gene (MGC16943), mRNA
NM_080661	Homo sapiens similar to RIKEN cDNA 0610008P16 gene (MGC15937), mRNA
NM_080658	Homo sapiens similar to RIKEN cDNA 0610006H10 gene (MGC9740), mRNA
NM_080656	Homo sapiens similar to RIKEN cDNA A430101B06 gene (MGC13017), mRNA
NM_080651	Homo sapiens similar to RIKEN cDNA 1810038N03 gene (MGC9890), mRNA
NM_080650	Homo sapiens similar to RIKEN cDNA 5730421E18 gene (MGC14798), mRNA
NM_080604	Homo sapiens tight junction protein 4 (peripheral) (TJP4), mRNA
NM_080552	Homo sapiens vesicular inhibitory amino acid transporter (VIAAT), mRNA
NM_080429	Homo sapiens aquaporin 10 (AQP10), mRNA
NM_018897	Homo sapiens axonemal dynein heavy chain 7 (DNAH7), mRNA
NM_015570	Homo sapiens autism-related protein 1 (KIAA0442), mRNA
NM_015132	Homo sapiens sorting nexin 13 (SNX13), mRNA
NM_022457	Homo sapiens similar to constitutive photomorphogenic protein 1 (Arabidopsis) (FLJ10416), mRNA
NM_030658	Homo sapiens putative ankyrin-repeat containing protein (DKFZP564D166), mRNA
NM_058229	Homo sapiens F-box only protein 32 (FBXO32), mRNA
NM_058188	Homo sapiens chromosome 21 open reading frame 67 (C21orf67), mRNA
NM_058187	Homo sapiens chromosome 21 open reading frame 63 (C21orf63), mRNA
NM_058171	Homo sapiens ING1-like tumor suppressor protein (ING1-like), mRNA
NM_058167	Homo sapiens ubiquitin conjugating enzyme 6 (Ubc6p), mRNA
NM_015242	Homo sapiens centaurin, delta 2 (CENTD2), mRNA
NM_054114	Homo sapiens hypothetical protein FLJ32631 (FLJ32631), mRNA
NM_054111	Homo sapiens inositol hexaphosphate kinase 3 (IHPK3), mRNA

NM_054108	Homo sapiens H-rev107-like protein 5 (HRLP5), mRNA
NM_020794	Homo sapiens densin-180 (KIAA1365), mRNA
NM_054032	Homo sapiens G protein-coupled receptor MRGX4 (MRGX4), mRNA
NM_054031	Homo sapiens G protein-coupled receptor MRGX3 (MRGX3), mRNA
NM_054030	Homo sapiens G protein-coupled receptor MRGX2 (MRGX2), mRNA
NM_054023	Homo sapiens uteroglobin-related protein 1 (UGRP1), mRNA
NM_054024	Homo sapiens melanoma inhibitory activity protein 2 (MIA2), mRNA
NM_031946	Homo sapiens centaurin, gamma 3 (CENTG3), mRNA
NM_052860	Homo sapiens kruppel-like zinc finger protein (ZNF300), mRNA
NM_053054	Homo sapiens cation channel of sperm (CATSPER), mRNA
NM_053053	Homo sapiens SPT3-associated factor 42 (STAF42), mRNA
NM_053048	Homo sapiens hypothetical protein MGC16384 (MGC16384), mRNA
NM_053047	Homo sapiens hypothetical protein MGC16063 (MGC16063), mRNA
NM_053040	Homo sapiens PNAS-123 (LOC85028), mRNA
NM_053039	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B28 (UGT2B28), mRNA
NM_053001	Homo sapiens odd-skipped-related 2A protein (OSR2), mRNA
NM_052997	Homo sapiens breast cancer antigen NY-BR-1 (NY-BR-1), mRNA
NM_052971	Homo sapiens liver-expressed antimicrobial peptide 2 (LEAP-2), mRNA
NM_052956	Homo sapiens medium-chain acyl-CoA synthetase (MACS1), mRNA
NM_052942	Homo sapiens guanylate binding protein 5 (GBP5), mRNA
NM_052931	Homo sapiens activating NK receptor (KALI), mRNA
NM_052879	Homo sapiens c-Mpl binding protein (LOC113251), mRNA
NM_030928	Homo sapiens DNA replication factor (CDT1), mRNA
NM_025185	Homo sapiens putative ankyrin-repeat containing protein (DKFZP564D166), mRNA
NM_015179	Homo sapiens KIAA0690 protein (KIAA0690), mRNA
NM_033626	Homo sapiens JM11 protein (JM11), mRNA
NM_022735	Homo sapiens golgi phosphoprotein 1 (GOLPH1), mRNA
NM_033547	Homo sapiens hypothetical gene MGC16733 similar to CG12113 (MGC16733), mRNA
NM_032268	Homo sapiens nerve injury gene 283 (NIN283), mRNA
NM_016167	Homo sapiens retinoic acid repressible protein (RARG-1), mRNA
NM_033414	Homo sapiens hypothetical protein MGC17552 (MGC17552), mRNA
NM_016336	Homo sapiens non-canonical ubquitin conjugating enzyme 1 (NCUBE1), mRNA
NM_033317	Homo sapiens hypothetical gene ZD52F10 (ZD52F10), mRNA
NM_033266	Homo sapiens ER to nucleus signalling 2 (ERN2), mRNA
NM_031955	Homo sapiens NYD-SP12 protein (NYD-SP12), mRNA
NM_033210	Homo sapiens hypothetical protein FLJ14855 (FLJ14855), mRNA
NM_033211	Homo sapiens hypothetical gene supported by AF038182; BC009203 (LOC90355), mRNA
NM_033194	Homo sapiens small heat shock protein B9 (HspB9), mRNA
NM_032122	Homo sapiens dystrobrevin binding protein 1 (DTNBP1), mRNA
NM_020405	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
NM_033115	Homo sapiens hypothetical protein MGC16169 (MGC16169), mRNA
NM_033117	Homo sapiens hypothetical protein MGC2734 (MGC2734), mRNA
NM_033103	Homo sapiens rhophilin-like protein (LOC85415), mRNA
NM_033035	Homo sapiens thymic stromal lymphopoietin (TSLP), mRNA
NM_014001	Homo sapiens golgi associated, gamma adaptin ear containing, ARF binding protein 3 (GGA3), mRNA
NM_015149	Homo sapiens RalGDS-like gene (RGL), mRNA
NM_032937	Homo sapiens AD038 (LOC85026), mRNA

NM_032932	Homo sapiens hypothetical protein MGC11316 (MGC11316), mRNA
NM_032930	Homo sapiens hypothetical protein MGC13040 (MGC13040), mRNA
NM_032918	Homo sapiens RAS-like, estrogen-regulated, growth-inhibitor (RERG), mRNA
NM_032916	Homo sapiens hypothetical protein MGC16279 (MGC16279), mRNA
NM_032907	Homo sapiens hypothetical protein MGC14421 (MGC14421), mRNA
NM_032904	Homo sapiens hypothetical protein MGC14433 (MGC14433), mRNA
NM_032900	Homo sapiens hypothetical protein MGC14258 (MGC14258), mRNA
NM_032895	Homo sapiens hypothetical protein MGC14376 (MGC14376), mRNA
NM_032888	Homo sapiens KIAA1870 protein (KIAA1870), mRNA
NM_032886	Homo sapiens hypothetical protein MGC15912 (MGC15912), mRNA
NM_032884	Homo sapiens hypothetical protein MGC15882 (MGC15882), mRNA
NM_032876	Homo sapiens hypothetical protein MGC15563 (MGC15563), mRNA
NM_032875	Homo sapiens hypothetical protein MGC15482 (MGC15482), mRNA
NM_032874	Homo sapiens hypothetical protein MGC15438 (MGC15438), mRNA
NM_032872	Homo sapiens NADPH oxidase-related, C2 domain-containing protein (JFC1), mRNA
NM_032871	Homo sapiens tumor necrosis factor receptor superfamily, member 19-like (TNFRSF19L), mRNA
NM_032866	Homo sapiens hypothetical protein FLJ14957 (FLJ14957), mRNA
NM_032860	Homo sapiens hypothetical protein FLJ14909 (FLJ14909), mRNA
NM_032858	Homo sapiens hypothetical protein FLJ14904 (FLJ14904), mRNA
NM_032852	Homo sapiens AUT-like 1, cysteine endopeptidase (S. cerevisiae) (AUTL1), mRNA
NM_032848	Homo sapiens hypothetical protein FLJ14827 (FLJ14827), mRNA
NM_032845	Homo sapiens hypothetical protein FLJ14816 (FLJ14816), mRNA
NM_032835	Homo sapiens hypothetical protein FLJ14761 (FLJ14761), mRNA
NM_032824	Homo sapiens hypothetical protein FLJ14681 (FLJ14681), mRNA
NM_032823	Homo sapiens hypothetical protein FLJ14675 (FLJ14675), mRNA
NM_032822	Homo sapiens hypothetical protein FLJ14668 (FLJ14668), mRNA
NM_032818	Homo sapiens hypothetical protein FLJ14642 (FLJ14642), mRNA
NM_032804	Homo sapiens hypothetical protein FLJ14547 (FLJ14547), mRNA
NM_032795	Homo sapiens hypothetical protein FLJ14494 (FLJ14494), mRNA
NM_032783	Homo sapiens hypothetical protein FLJ14431 (FLJ14431), mRNA
NM_032766	Homo sapiens hypothetical protein MGC16179 (MGC16179), mRNA
NM_032763	Homo sapiens hypothetical protein MGC16142 (MGC16142), mRNA
NM_032756	Homo sapiens hypothetical protein MGC15668 (MGC15668), mRNA
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NM_032720	Homo sapiens hypothetical protein MGC10724 (MGC10724), mRNA
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NM_032667	Homo sapiens hypothetical protein MGC4694 (MGC4694), mRNA
NM_032661	Homo sapiens hypothetical protein MGC5139 (MGC5139), mRNA
NM_032634	Homo sapiens hypothetical protein MGC3079 (MGC3079), mRNA

NM_032631	Homo sapiens hypothetical protein MGC2641 (MGC2641), mRNA
NM_032601	Homo sapiens methylmalonyl CoA epimerase (MCEE), mRNA
NM_032596	Homo sapiens testes development-related NYD-SP22 (NYD-SP22), mRNA
NM_032593	Homo sapiens PKCI-1-related HIT protein (HIT-17), mRNA
NM_032586	Homo sapiens testis transcript Y 8 (TTY8), mRNA
NM_032582	Homo sapiens ubiquitin specific protease (NY-REN-60), mRNA
NM_032580	Homo sapiens hairy and enhancer of split 7 (Drosophila) (HES7), mRNA
NM_032574	Homo sapiens dpy-30-like protein (LOC84661), mRNA
NM_032558	Homo sapiens hypothetical protein FLJ14753 (FLJ14753), mRNA
NM_032557	Homo sapiens HP43.8KD protein (HP43.8KD), mRNA
NM_032553	Homo sapiens putative purinergic receptor (FKSG79), mRNA
NM_032545	Homo sapiens cryptic gene (CRYPTIC), mRNA
NM_020963	Homo sapiens Mov10, Moloney leukemia virus 10, homolog (mouse) (MOV10), mRNA
NM_032522	Homo sapiens hypothetical protein MGC2629 (MGC2629), mRNA
NM_032507	Homo sapiens cerebral protein-4 (HUCEP-4), mRNA
NM_032499	Homo sapiens hypothetical protein HH114 (HH114), mRNA
NM_032494	Homo sapiens zinc finger protein (LOC84524), mRNA
NM_032492	Homo sapiens hypothetical protein GL009 (GL009), mRNA
NM_032487	Homo sapiens actin related protein M1 (ARPM1), mRNA
NM_032486	Homo sapiens dynactin 4 (MGC3248), mRNA
NM_032445	Homo sapiens MEGF11 protein (MEGF11), mRNA
NM_030898	Homo sapiens hypothetical protein FLJ21673 (FLJ21673), mRNA
NM_032412	Homo sapiens putative nuclear protein ORF1-FL49 (ORF1-FL49), mRNA
NM_032411	Homo sapiens esophageal cancer related gene 4 protein (ECRG4), mRNA
NM_015247	Homo sapiens cylindromatosis (turban tumor syndrome) (CYLD), mRNA
NM_032330	Homo sapiens hypothetical protein MGC12536 (MGC12536), mRNA
NM_032384	Homo sapiens hypothetical protein FLJ23183 (FLJ23183), mRNA
NM_032372	Homo sapiens hypothetical protein MGC16186 (MGC16186), mRNA
NM_032367	Homo sapiens hypothetical protein MGC15435 (MGC15435), mRNA
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NM_032288	Homo sapiens hypothetical protein DKFZp761B1514 (DKFZp761B1514), mRNA
NM_032273	Homo sapiens hypothetical protein DKFZp586C1924 (DKFZp586C1924),

	mRNA
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NM_032267	Homo sapiens hypothetical protein DKFZp434E169 (DKFZp434E169), mRNA
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NM_032261	Homo sapiens hypothetical protein DKFZp434N0650 (DKFZp434N0650), mRNA
NM_032258	Homo sapiens hypothetical protein DKFZp434P2235 (DKFZp434P2235), mRNA
NM_032251	Homo sapiens hypothetical protein DKFZp434G0920 (DKFZp434G0920), mRNA
NM_032250	Homo sapiens hypothetical protein DKFZp434A171 (DKFZp434A171), mRNA
NM_032249	Homo sapiens hypothetical protein DKFZp434F1819 (DKFZp434F1819), mRNA
NM_032248	Homo sapiens hypothetical protein DKFZp434F1719 (DKFZp434F1719), mRNA
NM_032246	Homo sapiens hypothetical protein DKFZp434J0617 (DKFZp434J0617), mRNA
NM_032245	Homo sapiens hypothetical protein DKFZp434I1916 (DKFZp434I1916), mRNA
NM_032223	Homo sapiens hypothetical protein FLJ22427 (FLJ22427), mRNA
NM_032209	Homo sapiens hypothetical protein FLJ21777 (FLJ21777), mRNA
NM_032193	Homo sapiens hypothetical protein FLJ20974 (FLJ20974), mRNA
NM_032177	Homo sapiens hypothetical protein FLJ13193 (FLJ13193), mRNA
NM_032167	Homo sapiens hypothetical protein FLJ12363 (FLJ12363), mRNA
NM_032161	Homo sapiens KIAA1870 protein (KIAA1870), mRNA
NM_032154	Homo sapiens MBLR protein (MBLR), mRNA
NM_032151	Homo sapiens hypothetical protein DKFZp566K1946 (DKFZP566K1946), mRNA
NM_032148	Homo sapiens hypothetical protein DKFZp434K0427 (DKFZP434K0427), mRNA
NM_032139	Homo sapiens hypothetical protein DKFZp434L0718 (DKFZP434L0718), mRNA
NM_032138	Homo sapiens hypothetical protein DKFZp434E2318 (DKFZP434E2318), mRNA
NM_032136	Homo sapiens hypothetical protein DKFZp434L1717 (DKFZP434L1717), mRNA
NM_032125	Homo sapiens hypothetical protein DKFZp564D0478 (DKFZP564D0478), mRNA
NM_032120	Homo sapiens hypothetical protein DKFZp564O0523 (DKFZP564O0523), mRNA
NM_020921	Homo sapiens ninein (GSK3B interacting protein) (NIN), mRNA
NM_020441	Homo sapiens hypothetical protein DKFZp762I166 (DKFZP762I166), mRNA
NM_018719	Homo sapiens hypothetical protein DKFZp762L0311 (DKFZp762L0311), mRNA
NM_015630	Homo sapiens DKFZP566F2124 protein (DKFZP566F2124), mRNA
NM_015621	Homo sapiens DKFZP434C171 protein (DKFZP434C171), mRNA
NM_015595	Homo sapiens DKFZP434D146 protein (DKFZP434D146), mRNA
NM_015496	Homo sapiens DKFZP434I116 protein (DKFZP434I116), mRNA
NM_015471	Homo sapiens DKFZP566O1646 protein (DC8), mRNA
NM_015453	Homo sapiens DKFZP434F091 protein (DKFZP434F091), mRNA
NM_015023	Homo sapiens KIAA1037 protein (KIAA1037), mRNA
NM_014972	Homo sapiens KIAA1049 protein (KIAA1049), mRNA
NM_032042	Homo sapiens hypothetical protein DKFZp564D172 (DKFZP564D172), mRNA
NM_032036	Homo sapiens TLH29 protein precursor (TLH29), mRNA

NM_032030	Homo sapiens FKSG83 (FKSG83), mRNA
NM_032028	Homo sapiens serine/threonine kinase FKSG81 (FKSG81), mRNA
NM_032025	Homo sapiens CDA02 protein (CDA02), mRNA
NM_032021	Homo sapiens AD031 protein (AD031), mRNA
NM_031944	Homo sapiens Mix-like homeobox protein 1 (MILD1), mRNA
NM_031920	Homo sapiens ARG99 protein (ARG99), mRNA
NM_031480	Homo sapiens hypothetical protein AD034 (AD034), mRNA
NM_031478	Homo sapiens hypothetical protein DKFZp434I2117 (DKFZP434I2117), mRNA
NM_031477	Homo sapiens hypothetical protein MGC10500 (MGC10500), mRNA
NM_031476	Homo sapiens hypothetical protein DKFZp434B044 (DKFZP434B044), mRNA
NM_031472	Homo sapiens hypothetical protein MGC11134 (MGC11134), mRNA
NM_031471	Homo sapiens hypothetical protein MGC10966 (MGC10966), mRNA
NM_031457	Homo sapiens membrane-spanning 4-domains, subfamily A, member 8B (MS4A8B), mRNA
NM_031450	Homo sapiens hypothetical protein p5326 (P5326), mRNA
NM_031443	Homo sapiens hypothetical protein MGC4607 (MGC4607), mRNA
NM_031438	Homo sapiens hypothetical protein DKFZp761I172 (DKFZP761I172), mRNA
NM_031434	Homo sapiens hypothetical protein MGC5442 (MGC5442), mRNA
NM_031418	Homo sapiens chromosome 11 open reading frame 25 (C11orf25), mRNA
NM_015497	Homo sapiens DKFZP564G2022 protein (DKFZP564G2022), mRNA
NM_031306	Homo sapiens hypothetical protein DKFZp564B1023 (DKFZP564B1023), mRNA
NM_031295	Homo sapiens hypothetical protein PP1226 (PP1226), mRNA
NM_031291	Homo sapiens hypothetical protein DKFZp434N1235 (DKFZP434N1235), mRNA
NM_031290	Homo sapiens hypothetical protein DKFZp434K1172 (DKFZP434K1172), mRNA
NM_031270	Homo sapiens PRO1596 protein (PRO1596), mRNA
NM_031268	Homo sapiens PRO0461 protein (PRO0461), mRNA
NM_031217	Homo sapiens hypothetical protein DKFZp434G2226 (DKFZP434G2226), mRNA
NM_013358	Homo sapiens peptidylarginine deiminase type I (hPAD-colony10), mRNA
NM_030980	Homo sapiens hypothetical protein FLJ12671 (FLJ12671), mRNA
NM_030954	Homo sapiens hypothetical protein DKFZp564A022 (DKFZP564A022), mRNA
NM_030953	Homo sapiens hypothetical protein DKFZp761E2110 (DKFZP761E2110), mRNA
NM_030941	Homo sapiens exonuclease NEF-sp (LOC81691), mRNA
NM_030939	Homo sapiens hypothetical protein FLJ12619 (FLJ12619), mRNA
NM_030938	Homo sapiens likely ortholog of rat vacuole membrane protein 1 (VMP1), mRNA
NM_030932	Homo sapiens diaphanous homolog 3 (Drosophila) (DIAPH3), mRNA
NM_030927	Homo sapiens hypothetical protein MGC11352 (MGC11352), mRNA
NM_030925	Homo sapiens hypothetical protein FLJ12577 (FLJ12577), mRNA
NM_030918	Homo sapiens hypothetical protein My014 (MY014), mRNA
NM_030911	Homo sapiens protein kinase NYD-SP15 (NYD-SP15), mRNA
NM_030899	Homo sapiens hypothetical protein FLJ23407 (FLJ23407), mRNA
NM_018657	Homo sapiens myoneurin (MYNN), mRNA
NM_030818	Homo sapiens hypothetical protein MGC10471 (MGC10471), mRNA
NM_030813	Homo sapiens suppressor of potassium transport defect 3 (SKD3), mRNA
NM_030808	Homo sapiens LIS1-interacting protein NUDEL; endooligopeptidase A (NUDEL), mRNA
NM_030805	Homo sapiens hypothetical protein DKFZp564L2423 (DKFZP564L2423),

	mRNA
NM_030802	Homo sapiens C/EBP-induced protein (LOC81558), mRNA
NM_030800	Homo sapiens hypothetical protein DKFZp564O1664 (DKFZP564O1664), mRNA
NM_030799	Homo sapiens hypothetical protein AF140225 (AF140225), mRNA
NM_030793	Homo sapiens hypothetical protein SP329 (SP329), mRNA
NM_030792	Homo sapiens hypothetical protein PP1665 (PP1665), mRNA
NM_030780	Homo sapiens folate transporter/carrier (LOC81034), mRNA
NM_030674	Homo sapiens solute carrier family 38, member 1 (SLC38A1), mRNA
NM_030672	Homo sapiens hypothetical protein FLJ10312 (FLJ10312), mRNA
NM_024947	Homo sapiens hypothetical protein FLJ12729 (FLJ12729), mRNA
NM_024963	Homo sapiens hypothetical protein FLJ11467 (FLJ11467), mRNA
NM_017600	Homo sapiens hypothetical protein DKFZp434M0331 (DKFZp434M0331), mRNA
NM_030652	Homo sapiens NG3 protein (NG3), mRNA
NM_030651	Homo sapiens chromosome 6 open reading frame 31 (C6orf31), mRNA
NM_020444	Homo sapiens KIAA1191 protein (KIAA1191), mRNA
NM_024055	Homo sapiens hypothetical protein MGC5499 (MGC5499), mRNA
NM_025154	Homo sapiens KIAA0810 protein (KIAA0810), mRNA
NM_017515	Homo sapiens novel protein (HSNOV1), mRNA
NM_024924	Homo sapiens hypothetical protein FLJ12985 (FLJ12985), mRNA
NM_030579	Homo sapiens cytochrome b5 outer mitochondrial membrane precursor (CYB5-M), mRNA
NM_022068	Homo sapiens hypothetical protein FLJ23403 (FLJ23403), mRNA
NM_025179	Homo sapiens plexin A2 (PLXNA2), mRNA
NM_014033	Homo sapiens DKFZP586A0522 protein (DKFZP586A0522), mRNA
NM_006468	Homo sapiens polymerase (RNA) III (DNA directed) (62kD) (RPC62), mRNA
NM_025263	Homo sapiens CAT56 protein (CAT56), mRNA
NM_025262	Homo sapiens G5C protein (G5C), mRNA
NM_025261	Homo sapiens G6C protein (G6C), mRNA
NM_025260	Homo sapiens G6B protein (G6B), mRNA
NM_025259	Homo sapiens NG23 protein (NG23), mRNA
NM_025258	Homo sapiens NG37 protein (G7C), mRNA
NM_025231	Homo sapiens hypothetical protein FLJ22191 (FLJ22191), mRNA
NM_025226	Homo sapiens MSTP032 protein (MSTP032), mRNA
NM_025211	Homo sapiens protein kinase anchoring protein GKAP42 (GKAP42), mRNA
NM_025201	Homo sapiens hypothetical protein PP1628 (PP1628), mRNA
NM_025192	Homo sapiens hypothetical protein FLJ23071 (FLJ23071), mRNA
NM_025188	Homo sapiens hypothetical protein FLJ13181 (FLJ13181), mRNA
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NM_025165	Homo sapiens hypothetical protein FLJ22637 (FLJ22637), mRNA
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NM_025151	Homo sapiens hypothetical protein FLJ22622 (FLJ22622), mRNA
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NM_025144	Homo sapiens hypothetical protein FLJ22670 (FLJ22670), mRNA
NM_025138	Homo sapiens hypothetical protein FLJ12661 (FLJ12661), mRNA
NM_025126	Homo sapiens ring finger protein 34 (RNF34), mRNA
NM_025125	Homo sapiens hypothetical protein FLJ13263 (FLJ13263), mRNA
NM_025124	Homo sapiens hypothetical protein FLJ21749 (FLJ21749), mRNA
NM_025109	Homo sapiens hypothetical protein FLJ22865 (FLJ22865), mRNA
NM_025099	Homo sapiens hypothetical protein FLJ22170 (FLJ22170), mRNA

NM_025098	Homo sapiens hypothetical protein FLJ22644 (FLJ22644), mRNA
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NM_025077	Homo sapiens hypothetical protein FLJ13949 (FLJ13949), mRNA
NM_025076	Homo sapiens hypothetical protein FLJ23591 (FLJ23591), mRNA
NM_025072	Homo sapiens chromosome 9 open reading frame 15 (C9orf15), mRNA
NM_025070	Homo sapiens hypothetical protein FLJ22242 (FLJ22242), mRNA
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NM_024976	Homo sapiens hypothetical protein FLJ11996 (FLJ11996), mRNA
NM_024956	Homo sapiens hypothetical protein FLJ23375 (FLJ23375), mRNA
NM_024944	Homo sapiens chromosome 21 open reading frame 68 (C21orf68), mRNA
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NM_024841	Homo sapiens hypothetical protein FLJ14213 (FLJ14213), mRNA
NM_024839	Homo sapiens hypothetical protein FLJ22638 (FLJ22638), mRNA
NM_024837	Homo sapiens hypothetical protein FLJ21472 (FLJ21472), mRNA
NM_024835	Homo sapiens C3HC4-type zinc finger protein (LZK1), mRNA
NM_024815	Homo sapiens hypothetical protein FLJ22494 (FLJ22494), mRNA

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NM_024754	Homo sapiens hypothetical protein FLJ12598 (FLJ12598), mRNA
NM_024749	Homo sapiens hypothetical protein FLJ12505 (FLJ12505), mRNA
NM_024746	Homo sapiens hypothetical protein FLJ13840 (FLJ13840), mRNA
NM_024732	Homo sapiens hypothetical protein FLJ14351 (FLJ14351), mRNA
NM_024731	Homo sapiens chromosome 16 open reading frame 44 (C16orf44), mRNA
NM_024727	Homo sapiens hypothetical protein FLJ23259 (FLJ23259), mRNA
NM_024722	Homo sapiens hypothetical protein FLJ13322 (FLJ13322), mRNA
NM_024717	Homo sapiens hypothetical protein FLJ22344 (FLJ22344), mRNA
NM_024715	Homo sapiens hypothetical protein FLJ22625 (FLJ22625), mRNA
NM_024709	Homo sapiens hypothetical protein FLJ14146 (FLJ14146), mRNA
NM_024705	Homo sapiens hypothetical protein FLJ13639 (FLJ13639), mRNA
NM_024703	Homo sapiens hypothetical protein FLJ22593 (FLJ22593), mRNA
NM_024701	Homo sapiens ankyrin repeat and SOCS box-containing 13 (ASB13), mRNA
NM_024700	Homo sapiens Smad nuclear interacting protein (SNIP1), mRNA
NM_024695	Homo sapiens hypothetical protein FLJ13993 (FLJ13993), mRNA
NM_024693	Homo sapiens hypothetical protein FLJ20909 (FLJ20909), mRNA
NM_024688	Homo sapiens hypothetical protein FLJ13031 (FLJ13031), mRNA
NM_024686	Homo sapiens hypothetical protein FLJ23033 (FLJ23033), mRNA
NM_024678	Homo sapiens hypothetical protein FLJ23441 (FLJ23441), mRNA
NM_024675	Homo sapiens hypothetical protein FLJ21816 (FLJ21816), mRNA
NM_024672	Homo sapiens hypothetical protein FLJ23320 (FLJ23320), mRNA
NM_024666	Homo sapiens hypothetical protein FLJ11506 (FLJ11506), mRNA
NM_024654	Homo sapiens hypothetical protein FLJ23323 (FLJ23323), mRNA
NM_024650	Homo sapiens hypothetical protein FLJ22531 (FLJ22531), mRNA
NM_024649	Homo sapiens hypothetical protein FLJ23590 (FLJ23590), mRNA
NM_024647	Homo sapiens hypothetical protein FLJ13287 (FLJ13287), mRNA
NM_024640	Homo sapiens hypothetical protein FLJ23476 (FLJ23476), mRNA
NM_024636	Homo sapiens likely ortholog of mouse tumor necrosis-alpha-induced adipose-related protein (FLJ23153), mRNA
NM_024628	Homo sapiens hypothetical protein FLJ23188 (FLJ23188), mRNA
NM_024627	Homo sapiens hypothetical protein FLJ21125 (FLJ21125), mRNA
NM_024626	Homo sapiens hypothetical protein FLJ22418 (FLJ22418), mRNA
NM_024624	Homo sapiens hypothetical protein FLJ22116 (FLJ22116), mRNA
NM_024616	Homo sapiens hypothetical protein FLJ23186 (FLJ23186), mRNA
NM_024615	Homo sapiens hypothetical protein FLJ21308 (FLJ21308), mRNA

NM_024613	Homo sapiens phafin 2 (FLJ13187), mRNA
NM_024610	Homo sapiens hypothetical protein FLJ22623 (FLJ22623), mRNA
NM_024609	Homo sapiens hypothetical protein FLJ21841 (FLJ21841), mRNA
NM_024606	Homo sapiens hypothetical protein FLJ11756 (FLJ11756), mRNA
NM_024605	Homo sapiens hypothetical protein FLJ20896 (FLJ20896), mRNA
NM_024602	Homo sapiens hypothetical protein FLJ21156 (FLJ21156), mRNA
NM_024595	Homo sapiens hypothetical protein FLJ12666 (FLJ12666), mRNA
NM_024585	Homo sapiens hypothetical protein FLJ22160 (FLJ22160), mRNA
NM_024584	Homo sapiens hypothetical protein FLJ13646 (FLJ13646), mRNA
NM_024580	Homo sapiens hypothetical protein FLJ13119 (FLJ13119), mRNA
NM_024570	Homo sapiens hypothetical protein FLJ11712 (FLJ11712), mRNA
NM_024565	Homo sapiens hypothetical protein FLJ14166 (FLJ14166), mRNA
NM_024556	Homo sapiens hypothetical protein FLJ21103 (FLJ21103), mRNA
NM_024552	Homo sapiens hypothetical protein FLJ12089 (FLJ12089), mRNA
NM_024546	Homo sapiens hypothetical protein FLJ13449 (FLJ13449), mRNA
NM_024534	Homo sapiens hypothetical protein FLJ12684 (FLJ12684), mRNA
NM_024532	Homo sapiens hypothetical protein FLJ22724 (FLJ22724), mRNA
NM_024526	Homo sapiens hypothetical protein FLJ21522 (FLJ21522), mRNA
NM_024523	Homo sapiens hypothetical protein FLJ22035 (FLJ22035), mRNA
NM_024522	Homo sapiens hypothetical protein FLJ12650 (FLJ12650), mRNA
NM_024516	Homo sapiens hypothetical protein MGC4606 (MGC4606), mRNA
NM_024514	Homo sapiens hypothetical protein MGC4663 (MGC4663), mRNA
NM_024507	Homo sapiens hypothetical protein MGC10791 (MGC10791), mRNA
NM_015288	Homo sapiens KIAA0239 protein (KIAA0239), mRNA
NM_024419	Homo sapiens Phosphatidylglycerophosphate Synthase (PGS1), mRNA
NM_024345	Homo sapiens hypothetical protein MGC10765 (MGC10765), mRNA
NM_024340	Homo sapiens hypothetical protein MGC4179 (MGC4179), mRNA
NM_024330	Homo sapiens hypothetical protein MGC4365 (MGC4365), mRNA
NM_024326	Homo sapiens hypothetical protein MGC11279 (MGC11279), mRNA
NM_024321	Homo sapiens hypothetical protein MGC10433 (MGC10433), mRNA
NM_024312	Homo sapiens hypothetical protein MGC4170 (MGC4170), mRNA
NM_024308	Homo sapiens hypothetical protein MGC4172 (MGC4172), mRNA
NM_024307	Homo sapiens hypothetical protein MGC4171 (MGC4171), mRNA
NM_024295	Homo sapiens hypothetical protein MGC3067 (MGC3067), mRNA
NM_020062	Homo sapiens SLC2A4 regulator (SLC2A4RG), mRNA
NM_018491	Homo sapiens COBW-like protein (LOC55871), mRNA
NM_024116	Homo sapiens hypothetical protein MGC5306 (MGC5306), mRNA
NM_024114	Homo sapiens hypothetical protein MGC4827 (MGC4827), mRNA
NM_024113	Homo sapiens hypothetical protein MGC4707 (MGC4707), mRNA
NM_024099	Homo sapiens hypothetical protein MGC2477 (MGC2477), mRNA
NM_024092	Homo sapiens hypothetical protein MGC5508 (MGC5508), mRNA
NM_024084	Homo sapiens hypothetical protein MGC3196 (MGC3196), mRNA
NM_024072	Homo sapiens hypothetical protein MGC2835 (MGC2835), mRNA
NM_024067	Homo sapiens hypothetical protein MGC2718 (MGC2718), mRNA
NM_024063	Homo sapiens hypothetical protein MGC5347 (MGC5347), mRNA
NM_024040	Homo sapiens hypothetical protein MGC2491 (MGC2491), mRNA
NM_024036	Homo sapiens hypothetical protein MGC3103 (MGC3103), mRNA
NM_015450	Homo sapiens protection of telomeres 1 (POT1), mRNA
NM_021249	Homo sapiens sorting nexin 6 (SNX6), mRNA
NM_023932	Homo sapiens hypothetical protein MGC2487 (MGC2487), mRNA
NM_023930	Homo sapiens hypothetical protein MGC2376 (MGC2376), mRNA

NM_014045	Homo sapiens DKFZP564C1940 protein (DKFZP564C1940), mRNA
NM_015533	Homo sapiens DKFZP586B1621 protein (DKFZP586B1621), mRNA
NM_023927	Homo sapiens hypothetical protein FLJ21313 (FLJ21313), mRNA
NM_023923	Homo sapiens hypothetical protein FLJ13171 (FLJ13171), mRNA
NM_019054	Homo sapiens hypothetical protein MGC5560 (MGC5560), mRNA
NM_023070	Homo sapiens hypothetical protein (LOC65243), mRNA
NM_023015	Homo sapiens hypothetical protein FLJ21919 (FLJ21919), mRNA
NM_022899	Homo sapiens likely ortholog of mouse actin-related protein 8 homolog (S. cerevisiae) (FLJ12934), mRNA
NM_022836	Homo sapiens DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae) (DCLRE1B), mRNA
NM_022831	Homo sapiens hypothetical protein FLJ12806 (FLJ12806), mRNA
NM_022828	Homo sapiens hypothetical protein FLJ21940 (FLJ21940), mRNA
NM_022822	Homo sapiens hypothetical protein FLJ12387 similar to kinesin light chain (FLJ12387), mRNA
NM_022784	Homo sapiens hypothetical protein FLJ12476 (FLJ12476), mRNA
NM_022783	Homo sapiens hypothetical protein FLJ12428 (FLJ12428), mRNA
NM_022774	Homo sapiens hypothetical protein FLJ21144 (FLJ21144), mRNA
NM_022765	Homo sapiens hypothetical protein FLJ11937 (FLJ11937), mRNA
NM_022764	Homo sapiens hypothetical protein FLJ12998 (FLJ12998), mRNA
NM_022758	Homo sapiens hypothetical protein FLJ22195 (FLJ22195), mRNA
NM_022753	Homo sapiens hypothetical protein FLJ12903 (FLJ12903), mRNA
NM_022749	Homo sapiens retinoic acid induced 16 (RAI16), mRNA
NM_022746	Homo sapiens hypothetical protein FLJ22390 (FLJ22390), mRNA
NM_022728	Homo sapiens neurogenic differentiation 6 (NEUROD6), mRNA
NM_022496	Homo sapiens hypothetical protein FLJ13433 (FLJ13433), mRNA
NM_022490	Homo sapiens hypothetical protein FLJ13390 similar to PAF53 (FLJ13390), mRNA
NM_022484	Homo sapiens hypothetical protein FLJ13576 (FLJ13576), mRNA
NM_022483	Homo sapiens hypothetical protein FLJ21657 (FLJ21657), mRNA
NM_022473	Homo sapiens zinc finger protein 106 (ZFP106), mRNA
NM_022471	Homo sapiens hypothetical protein FLJ13057 similar to germ cell-less (FLJ13057), mRNA
NM_022463	Homo sapiens nucleoredoxin 1 (NXN), mRNA
NM_022462	Homo sapiens hypothetical protein FLJ14033 similar to hypoxia inducible factor 3, alpha subunit (HIF-3A), mRNA
NM_022461	Homo sapiens hypothetical protein FLJ21939 similar to 5-azacytidine induced gene 2 (FLJ21939), mRNA
NM_022453	Homo sapiens ring finger protein 25 (RNF25), mRNA
NM_022374	Homo sapiens likely ortholog of mouse ADP-ribosylation-like factor 6 interacting protein 2 (FLJ23293), mRNA
NM_022371	Homo sapiens ATP-dependant interferon responsive (ADIR), mRNA
NM_022369	Homo sapiens hypothetical protein FLJ12541 similar to Stra6 (FLJ12541), mRNA
NM_022367	Homo sapiens hypothetical protein FLJ12287 similar to semaphorins (FLJ12287), mRNA
NM_022359	Homo sapiens similar to rat myomegalin (LOC64182), mRNA
NM_022356	Homo sapiens growth suppressor 1 (GROS1), mRNA
NM_022354	Homo sapiens spermatogenesis associated 1 (SPATA1), mRNA
NM_022347	Homo sapiens IFRG15 protein (IFRG15), mRNA
NM_022341	Homo sapiens peptide deformylase-like protein (LOC64146), mRNA
NM_022164	Homo sapiens P3ECSL (LIECG3), mRNA

NM_022147	Homo sapiens 28kD interferon responsive protein (IFRG28), mRNA
NM_022140	Homo sapiens erythrocyte protein band 4.1-like 4 (EPB41L4), mRNA
NM_022133	Homo sapiens sorting nexin 16 (SNX16), mRNA
NM_022126	Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), mRNA
NM_022097	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC63928), mRNA
NM_022094	Homo sapiens hypothetical protein FLJ20871 similar to FSP27 (FLJ20871), mRNA
NM_022090	Homo sapiens transposon-derived Buster3 transposase-like (LOC63920), mRNA
NM_022074	Homo sapiens hypothetical protein FLJ22794 (FLJ22794), mRNA
NM_022071	Homo sapiens hypothetical protein FLJ20967 (FLJ20967), mRNA
NM_022063	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
NM_022060	Homo sapiens hypothetical protein FLJ12816 (FLJ12816), mRNA
NM_022034	Homo sapiens estrogen regulated gene 1 (ERG-1), mRNA
NM_021945	Homo sapiens hypothetical protein FLJ22174 (FLJ22174), mRNA
NM_021944	Homo sapiens hypothetical protein FLJ12154 (FLJ12154), mRNA
NM_021941	Homo sapiens hypothetical protein FLJ21324 (FLJ21324), mRNA
NM_021928	Homo sapiens hypothetical protein FLJ22649 similar to signal peptidase SPC22/23 (FLJ22649), mRNA
NM_021927	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
NM_021925	Homo sapiens hypothetical protein FLJ21820 (FLJ21820), mRNA
NM_021825	Homo sapiens hypothetical protein MDS025 (MDS025), mRNA
NM_015622	Homo sapiens CGI-43 protein (LOC51622), mRNA
NM_021639	Homo sapiens hypothetical protein SP192 (SP192), mRNA
NM_021637	Homo sapiens hypothetical protein FLJ14084 (FLJ14084), mRNA
NM_021614	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 (KCNN2), mRNA
NM_021182	Homo sapiens minor histocompatibility antigen HB-1 (HB-1), mRNA
NM_021170	Homo sapiens bHLH factor Hes4 (LOC57801), mRNA
NM_021146	Homo sapiens angiopoietin-like factor (CDT6), mRNA
NM_005146	Homo sapiens squamous cell carcinoma antigen recognised by T cells (SART1), mRNA
NM_021079	Homo sapiens N-myristoyltransferase 1 (NMT1), mRNA
NM_021046	Homo sapiens UHS KerB (LOC57830), mRNA
NM_021018	Homo sapiens H3 histone family, member I (H3FI), mRNA
NM_006643	Homo sapiens serologically defined colon cancer antigen 3 (SDCCAG3), mRNA
NM_017569	Homo sapiens transcription factor (p38 interacting protein) (P38IP), mRNA
NM_015239	Homo sapiens KIAA1035 protein (KIAA1035), mRNA
NM_014977	Homo sapiens KIAA0670 protein/acinus (KIAA0670), mRNA
NM_015176	Homo sapiens KIAA0483 protein (KIAA0483), mRNA
NM_014610	Homo sapiens KIAA0088 protein (KIAA0088), mRNA
NM_015516	Homo sapiens hypothetical protein, estradiol-induced (E2IG4), mRNA
NM_015388	Homo sapiens DKFZP566C243 protein (DKFZP566C243), mRNA
NM_015679	Homo sapiens hypothetical protein (CLONE24922), mRNA
NM_014409	Homo sapiens TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65 kD (TAF5L), mRNA
NM_014368	Homo sapiens LIM homeobox protein 6 (LHX6), mRNA
NM_014315	Homo sapiens host cell factor homolog (LCP), mRNA
NM_012414	Homo sapiens rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-GAP150), mRNA
NM_012219	Homo sapiens muscle RAS oncogene homolog (MRAS), mRNA
NM_007375	Homo sapiens TAR DNA binding protein (TARDBP), mRNA

NM_007074	Homo sapiens coronin, actin binding protein, 1A (CORO1A), mRNA
NM_006927	Homo sapiens sialyltransferase 4B (beta-galactosidase alpha-2,3-sialytransferase) (SIAT4B), mRNA
NM_006861	Homo sapiens RAB35, member RAS oncogene family (RAB35), mRNA
NM_006502	Homo sapiens polymerase (DNA directed), eta (POLH), mRNA
NM_005710	Homo sapiens polyglutamine binding protein 1 (PQBP1), mRNA
NM_005168	Homo sapiens ras homolog gene family, member E (ARHE), mRNA
NM_004190	Homo sapiens lipase, gastric (LIPF), mRNA
NM_004132	Homo sapiens hyaluronan binding protein 2 (HABP2), mRNA
NM_004492	Homo sapiens general transcription factor IIA, 2 (12kD subunit) (GTF2A2), mRNA
NM_004824	Homo sapiens chromodomain protein, Y chromosome-like (CDYL), mRNA
NM_003969	Homo sapiens ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast) (UBE2M), mRNA
NM_002711	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle) (PPP1R3A), mRNA
NM_003847	Homo sapiens peroxisomal biogenesis factor 11A (PEX11A), mRNA
NM_002004	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase) (FDPS), mRNA
NM_019111	Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA
NM_002120	Homo sapiens major histocompatibility complex, class II, DO beta (HLA-DOB), mRNA
NM_002118	Homo sapiens major histocompatibility complex, class II, DM beta (HLA-DMB), mRNA
NM_002125	Homo sapiens major histocompatibility complex, class II, DR beta 5 (HLA-DRB5), mRNA
NM_021983	Homo sapiens major histocompatibility complex, class II, DR beta 4 (HLA-DRB4), mRNA
NM_022555	Homo sapiens major histocompatibility complex, class II, DR beta 3 (HLA-DRB3), mRNA
NM_005962	Homo sapiens MAX interacting protein 1 (MXI1), transcript variant 1, mRNA
NM_130439	Homo sapiens MAX interacting protein 1 (MXI1), transcript variant 2, mRNA
NM_080923	Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 4, mRNA
NM_080922	Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 3, mRNA
NM_080921	Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 2, mRNA
NM_130386	Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant I, mRNA
NM_030781	Homo sapiens collectin sub-family member 12 (COLEC12), transcript variant II, mRNA
NM_130778	Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant short, mRNA
NM_000494	Homo sapiens collagen, type XVII, alpha 1 (COL17A1), transcript variant long, mRNA
NM_001856	Homo sapiens collagen, type XVI, alpha 1 (COL16A1), mRNA
NM_001855	Homo sapiens collagen, type XV, alpha 1 (COL15A1), mRNA
NM_058166	Homo sapiens tripartite motif-containing 6 (TRIM6), mRNA
NM_002838	Homo sapiens protein tyrosine phosphatase, receptor type, C (PTPRC), transcript

	variant 1, mRNA
NM_130390	Homo sapiens tripartite motif-containing 34 (TRIM34), transcript variant 3, mRNA
NM_130389	Homo sapiens tripartite motif-containing 34 (TRIM34), transcript variant 2, mRNA
NM_021616	Homo sapiens tripartite motif-containing 34 (TRIM34), transcript variant 1, mRNA
NM_030950	Homo sapiens ret finger protein (RFP), transcript variant beta, mRNA
NM_130785	Homo sapiens TPTE and PTEN homologous inositol lipid phosphatase (TPIP), mRNA
NM_130784	Homo sapiens hypothetical gene supported by AY027807; AY027808 (LOC93426), mRNA
NM_130783	Homo sapiens similar to neuronal tetraspanin (LOC90139), mRNA
NM_130782	Homo sapiens regulator of G-protein signalling 18 (RGS18), mRNA
NM_130781	Homo sapiens (RAB24), mRNA
NM_130772	Homo sapiens S100Z protein (S100Z), mRNA
NM_130769	Homo sapiens glycoprotein alpha 2 (GPA2), mRNA
NM_130770	Homo sapiens 5-hydroxytryptamine receptor 3 subunit C (HTR3C), mRNA
NM_130768	Homo sapiens GASZ (GASZ), mRNA
NM_130767	Homo sapiens cytosolic acetyl-CoA hydrolase (CACH-1), mRNA
NM_130773	Homo sapiens caspr5 protein (caspr5), mRNA
NM_006510	Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA
NM_033554	Homo sapiens major histocompatibility complex, class II, DP alpha 1 (HLA-DPA1), mRNA
NM_033282	Homo sapiens opsin 4 (melanopsin) (OPN4), mRNA
NM_032035	Homo sapiens MSTP031 protein (MSTP031), mRNA
NM_017882	Homo sapiens ceroid-lipofuscinosis, neuronal 6, late infantile, variant (CLN6), mRNA
NM_006983	Homo sapiens matrix metalloproteinase 23B (MMP23B), mRNA
NM_005608	Homo sapiens protein tyrosine phosphatase, receptor type, C-associated protein (PTPRCAP), mRNA
NM_004659	Homo sapiens matrix metalloproteinase 23A (MMP23A), mRNA
NM_025091	Homo sapiens hypothetical protein FLJ13330 (FLJ13330), mRNA
NM_130759	Homo sapiens immunity associated protein 1 (IMAP1), mRNA
NM_019841	Homo sapiens transient receptor potential cation channel, subfamily V, member 5 (TRPV5), mRNA
NM_017584	Homo sapiens aldehyde reductase (aldose reductase) like 6 (ALDRL6), mRNA
NM_017436	Homo sapiens alpha 1,4-galactosyltransferase (A4GALT), mRNA
NM_006480	Homo sapiens regulator of G-protein signalling 14 (RGS14), mRNA
NM_013357	Homo sapiens purine-rich element binding protein G (PURG), mRNA
NM_016155	Homo sapiens matrix metalloproteinase 17 (membrane-inserted) (MMP17), mRNA
NM_002813	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 (PSMD9), mRNA
NM_024549	Homo sapiens hypothetical protein FLJ21127 (FLJ21127), mRNA
NM_130441	Homo sapiens dendritic cell lectin b (DLEC), mRNA
NM_015409	Homo sapiens E1A binding protein p400 (EP400), mRNA
NM_003702	Homo sapiens regulator of G-protein signalling 20 (RGS20), mRNA
NM_016113	Homo sapiens transient receptor potential cation channel, subfamily V, member 2 (TRPV2), mRNA
NM_015530	Homo sapiens likely ortholog of rat golgi stacking protein homolog GRASP55 (GRASP55), mRNA

NM_005873	Homo sapiens regulator of G-protein signalling 19 (RGS19), mRNA
NM_130469	Homo sapiens Jun dimerization protein 2 (jdp2), mRNA
NM_130468	Homo sapiens dermatan-4-sulfotransferase-1 (D4ST-1), mRNA
NM_130467	Homo sapiens PAGE-5 protein (PAGE-5), mRNA
NM_130463	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) (ATP6G), mRNA
NM_130459	Homo sapiens torsin family 2, member A (TOR2A), mRNA
NM_021070	Homo sapiens latent transforming growth factor beta binding protein 3 (LTBP3), mRNA
NM_020865	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 36 (DDX36), mRNA
NM_016304	Homo sapiens 60S ribosomal protein L30 isolog (LOC51187), mRNA
NM_130443	Homo sapiens dipeptidylpeptidase III (DPP3), transcript variant 2, mRNA
NM_005700	Homo sapiens dipeptidylpeptidase III (DPP3), transcript variant 1, mRNA
NM_018152	Homo sapiens chromosome 20 open reading frame 12 (C20orf12), mRNA
NM_006027	Homo sapiens exonuclease 1 (EXO1), transcript variant 1, mRNA
NM_003686	Homo sapiens exonuclease 1 (EXO1), transcript variant 3, mRNA
NM_130398	Homo sapiens exonuclease 1 (EXO1), transcript variant 2, mRNA
NM_002837	Homo sapiens protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA
NM_000775	Homo sapiens cytochrome P450, subfamily IIJ (arachidonic acid epoxygenase) polypeptide 2 (CYP2J2), mRNA
NM_053056	Homo sapiens cyclin D1 (PRAD1 parathyroid adenomatosis 1) (CCND1), mRNA
NM_012090	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 1, mRNA
NM_017625	Homo sapiens intelectin (ITLN), mRNA
NM_015839	Homo sapiens ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2), transcript variant SV3, mRNA
NM_015838	Homo sapiens ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2), transcript variant SV2, mRNA
NM_015837	Homo sapiens ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2), transcript variant SV1, mRNA
NM_002003	Homo sapiens ficolin (collagen/fibrinogen domain containing) 1 (FCN1), mRNA
NM_016327	Homo sapiens ureidopropionase, beta (UPB1), mRNA
NM_016328	Homo sapiens GTF2I repeat domain containing 1 (GTF2IRD1), transcript variant 1, mRNA
NM_004108	Homo sapiens ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2), transcript variant SV0, mRNA
NM_002318	Homo sapiens lysyl oxidase-like 2 (LOXL2), mRNA
NM_130396	Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 2, mRNA
NM_003880	Homo sapiens WNT1 inducible signaling pathway protein 3 (WISP3), transcript variant 1, mRNA
NM_003881	Homo sapiens WNT1 inducible signaling pathway protein 2 (WISP2), mRNA
NM_080838	Homo sapiens WNT1 inducible signaling pathway protein 1 (WISP1), transcript variant 2, mRNA
NM_003882	Homo sapiens WNT1 inducible signaling pathway protein 1 (WISP1), transcript variant 1, mRNA
NM_000651	Homo sapiens complement component (3b/4b) receptor 1, including Knops blood group system (CR1), transcript variant S, mRNA
NM_000573	Homo sapiens complement component (3b/4b) receptor 1, including Knops blood group system (CR1), transcript variant F, mRNA

NM_006069	Homo sapiens murine retrovirus integration site 1 homolog (MRVI1), transcript variant 1, mRNA
NM_130385	Homo sapiens murine retrovirus integration site 1 homolog (MRVI1), transcript variant 2, mRNA
NM_018492	Homo sapiens T-LAK cell-originated protein kinase (TOPK), mRNA
NM_002462	Homo sapiens myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA
NM_015920	Homo sapiens ribosomal protein S27-like (RPS27L), mRNA
NM_016183	Homo sapiens ribosomal protein, large, P0-like (RPLP0L), mRNA
NM_080746	Homo sapiens ribosomal protein L10-like (RPL10L), mRNA
NM_032236	Homo sapiens FLJ23277 protein (FLJ23277), mRNA
NM_032784	Homo sapiens thrombospondin (FLJ14440), mRNA
NM_080731	Homo sapiens intermediate filament-like MGC:2625 (DKFZP586I2223), transcript variant 3, mRNA
NM_080730	Homo sapiens intermediate filament-like MGC:2625 (DKFZP586I2223), transcript variant 2, mRNA
NM_015945	Homo sapiens ovarian cancer overexpressed 1 (OVCOV1), mRNA
NM_018018	Homo sapiens solute carrier family 38, member 4 (SLC38A4), mRNA
NM_022451	Homo sapiens AD24 protein (AD24), mRNA
NM_020830	Homo sapiens phosphoinositide-binding protein SR1 (FENS-1), mRNA
NM_033630	Homo sapiens SCAN domain containing 1 (SCAND1), transcript variant 2, mRNA
NM_016558	Homo sapiens SCAN domain containing 1 (SCAND1), transcript variant 1, mRNA
NM_015438	Homo sapiens intermediate filament-like MGC:2625 (DKFZP586I2223), transcript variant 1, mRNA
NM_007371	Homo sapiens bromodomain containing 3 (BRD3), mRNA
NM_005104	Homo sapiens bromodomain containing 2 (BRD2), mRNA
NM_005031	Homo sapiens FXYD domain containing ion transport regulator 1 (phospholemman) (FXYD1), transcript variant a, mRNA
NM_021902	Homo sapiens FXYD domain containing ion transport regulator 1 (phospholemman) (FXYD1), transcript variant b, mRNA
NM_014164	Homo sapiens FXYD domain-containing ion transport regulator 5 (FXYD5), mRNA
NM_002463	Homo sapiens myxovirus (influenza virus) resistance 2 (mouse) (MX2), mRNA
NM_014577	Homo sapiens bromodomain containing 1 (BRD1), mRNA
NM_021004	Homo sapiens peroxisomal short-chain alcohol dehydrogenase (humNRDR), mRNA
NM_020399	Homo sapiens PDZ/coiled-coil domain binding partner for the rho-family GTPase TC10 (PIST), mRNA
NM_017935	Homo sapiens hypothetical protein FLJ20706 (BANK), mRNA
NM_018244	Homo sapiens chromosome 20 open reading frame 44 (C20orf44), mRNA
NM_016100	Homo sapiens N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae) (NAT5), mRNA
NM_016045	Homo sapiens chromosome 20 open reading frame 45 (C20orf45), mRNA
NM_007363	Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA
NM_002438	Homo sapiens mannose receptor, C type 1 (MRC1), mRNA
NM_015092	Homo sapiens PI-3-kinase-related kinase SMG-1 (SMG1), mRNA
NM_018993	Homo sapiens RAB5 interacting protein 2 (RIN2), mRNA
NM_080841	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), transcript variant 3, mRNA
NM_080840	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA),

	transcript variant 2, mRNA
NM_002836	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA), transcript variant 1, mRNA
NM_024832	Homo sapiens RAB5 interacting protein 3 (RIN3), mRNA
NM_023915	Homo sapiens G protein-coupled receptor 87 (GPR87), mRNA
NM_003029	Homo sapiens SHC (Src homology 2 domain containing) transforming protein 1 (SHC1), mRNA
NM_018490	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
NM_016020	Homo sapiens homolog of yeast mitochondrial transcription factor B (mtTFB), mRNA
NM_014475	Homo sapiens dihydrodiol dehydrogenase (dimeric) (DHDH), mRNA
NM_006065	Homo sapiens signal-regulatory protein beta 1 (SIRPB1), mRNA
NM_005527	Homo sapiens heat shock 70kD protein 1-like (HSPA1L), mRNA
NM_004648	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1), mRNA
NM_004480	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA
NM_003667	Homo sapiens G protein-coupled receptor 49 (GPR49), mRNA
NM_130434	Homo sapiens dipeptidylpeptidase 8 (DPP8), transcript variant 1, mRNA
NM_017743	Homo sapiens dipeptidylpeptidase 8 (DPP8), transcript variant 2, mRNA
NM_002122	Homo sapiens major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA
NM_006442	Homo sapiens DR1-associated protein 1 (negative cofactor 2 alpha) (DRAP1), mRNA
NM_080918	Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 2, nuclear gene encoding mitochondrial protein, mRNA
NM_080917	Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 3, nuclear gene encoding mitochondrial protein, mRNA
NM_080916	Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 1, nuclear gene encoding mitochondrial protein, mRNA
NM_080915	Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 5, nuclear gene encoding mitochondrial protein, mRNA
NM_001929	Homo sapiens deoxyguanosine kinase (DGUOK), transcript variant 4, nuclear gene encoding mitochondrial protein, mRNA
NM_080815	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 19, mRNA
NM_080814	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 18, mRNA
NM_080813	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 17, mRNA
NM_080812	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 16, mRNA
NM_080811	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 15, mRNA
NM_080810	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 14, mRNA
NM_080809	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 13, mRNA
NM_080808	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 12, mRNA
NM_080807	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 11, mRNA

NM_080806	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 10, mRNA
NM_080805	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 9, mRNA
NM_080804	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 8, mRNA
NM_080803	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 7, mRNA
NM_080802	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 6, mRNA
NM_080801	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 5, mRNA
NM_080800	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 4, mRNA
NM_080799	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 3, mRNA
NM_080798	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 2, mRNA
NM_005203	Homo sapiens collagen, type XIII, alpha 1 (COL13A1), transcript variant 1, mRNA
NM_004395	Homo sapiens drebrin 1 (DBN1), transcript variant 1, mRNA
NM_080881	Homo sapiens drebrin 1 (DBN1), transcript variant 2, mRNA
NM_080792	Homo sapiens brain-immunoglobulin-like molecule with tyrosine-based activation motifs (BIT), mRNA
NM_080816	Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 2, mRNA
NM_018556	Homo sapiens signal-regulatory protein beta 2 (SIRPB2), transcript variant 1, mRNA
NM_000787	Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase) (DBH), mRNA
NM_080426	Homo sapiens GNAS complex locus (GNAS), transcript variant 2, mRNA
NM_080425	Homo sapiens GNAS complex locus (GNAS), transcript variant 3, mRNA
NM_000516	Homo sapiens GNAS complex locus (GNAS), transcript variant 1, mRNA
NM_006571	Homo sapiens novel RGD-containing protein (WS-3), mRNA
NM_080926	Homo sapiens hypothetical protein similar to KIAA0187 gene product (LOC96610), mRNA
NM_080924	Homo sapiens hypothetical protein similar to CGI-67 protein (LOC91219), mRNA
NM_080925	Homo sapiens hypothetical protein similar to topoisomerase (DNA) III beta (H. sapiens) (LOC129020), mRNA
NM_080914	Homo sapiens asialoglycoprotein receptor 2 (ASGR2), transcript variant 3, mRNA
NM_080913	Homo sapiens asialoglycoprotein receptor 2 (ASGR2), transcript variant 2, mRNA
NM_080912	Homo sapiens asialoglycoprotein receptor 2 (ASGR2), transcript variant H2', mRNA
NM_001181	Homo sapiens asialoglycoprotein receptor 2 (ASGR2), transcript variant 1, mRNA
NM_001671	Homo sapiens asialoglycoprotein receptor 1 (ASGR1), mRNA
NM_005065	Homo sapiens sel-1 suppressor of lin-12-like (C. elegans) (SEL1L), mRNA
NM_014978	Homo sapiens VPS10 domain receptor protein SORCS 3 (SORCS3), mRNA
NM_015230	Homo sapiens centaurin, delta 1 (CENTD1), mRNA

NM_052868	Homo sapiens immunoglobulin superfamily, member 8 (IGSF8), mRNA
NM_032782	Homo sapiens hypothetical protein FLJ14428 (TIM3), mRNA
NM_032309	Homo sapiens chromosome 2 open reading frame 9 (C2orf9), mRNA
NM_021625	Homo sapiens transient receptor potential cation channel, subfamily V, member 4 (TRPV4), mRNA
NM_020960	Homo sapiens G protein-coupled receptor 107 (GPR107), mRNA
NM_024503	Homo sapiens human immunodeficiency virus type I enhancer binding protein 3 (HIVEP3), mRNA
NM_024112	Homo sapiens chromosome 9 open reading frame 16 (C9orf16), mRNA
NM_015192	Homo sapiens phospholipase C, beta 1 (phosphoinositide-specific) (PLCB1), mRNA
NM_022481	Homo sapiens ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3 (ARAP3), mRNA
NM_021634	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 7 (LGR7), mRNA
NM_013305	Homo sapiens sialyltransferase 8E (alpha-2, 8-polysialytransferase) (SIAT8E), mRNA
NM_019069	Homo sapiens WD repeat domain 5B (WDR5B), mRNA
NM_016179	Homo sapiens transient receptor potential cation channel, subfamily C, member 4 (TRPC4), mRNA
NM_016592	Homo sapiens GNAS complex locus (GNAS), transcript variant 4, mRNA
NM_014007	Homo sapiens zinc finger protein 297B (ZNF297B), mRNA
NM_012471	Homo sapiens transient receptor potential cation channel, subfamily C, member 5 (TRPC5), mRNA
NM_012459	Homo sapiens translocase of inner mitochondrial membrane 8 homolog B (yeast) (TIMM8B), mRNA
NM_004621	Homo sapiens transient receptor potential cation channel, subfamily C, member 6 (TRPC6), mRNA
NM_003304	Homo sapiens transient receptor potential cation channel, subfamily C, member 1 (TRPC1), mRNA
NM_002124	Homo sapiens major histocompatibility complex, class II, DR beta 1 (HLA-DRB1), mRNA
NM_000972	Homo sapiens ribosomal protein L7a (RPL7A), mRNA
NM_130384	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 6, mRNA
NM_033627	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 2, mRNA
NM_032166	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 5, mRNA
NM_024996	Homo sapiens mitochondrial elongation factor G (EFG1), mRNA
NM_033629	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 4, mRNA
NM_033628	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 3, mRNA
NM_016381	Homo sapiens three prime repair exonuclease 1 (TREX1), transcript variant 1, mRNA
NM_031892	Homo sapiens SH3-domain kinase binding protein 1 (SH3KBP1), mRNA
NM_003960	Homo sapiens N-acetyltransferase 8 (camello like) (NAT8), mRNA
NM_021093	Homo sapiens peptide YY, 2 (seminalplasmin) (PYY2), mRNA
NM_021092	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
NM_021190	Homo sapiens polypyrimidine tract binding protein 2 (PTBP2), mRNA
NM_013998	Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1,

	neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma) (TAC1), transcript variant delta, mRNA
NM_013997	Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma) (TAC1), transcript variant gamma, mRNA
NM_013996	Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma) (TAC1), transcript variant alpha, mRNA
NM_016235	Homo sapiens G protein-coupled receptor, family C, group 1, member B (GPRC5B), mRNA
NM_004630	Homo sapiens splicing factor 1 (SF1), mRNA
NM_000230	Homo sapiens leptin (obesity homolog, mouse) (LEP), mRNA
NM_003185	Homo sapiens TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135 kD (TAF4), mRNA
NM_003182	Homo sapiens tachykinin, precursor 1 (substance K, substance P, neurokinin 1, neurokinin 2, neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide gamma) (TAC1), transcript variant beta, mRNA
NM_002772	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA
NM_005857	Homo sapiens zinc metalloproteinase (STE24 homolog, yeast) (ZMPSTE24), mRNA
NM_006103	Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 1, mRNA
NM_080736	Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 2, mRNA
NM_080735	Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 5, mRNA
NM_080734	Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 4, mRNA
NM_080733	Homo sapiens WAP four-disulfide core domain 2 (WFDC2), transcript variant 3, mRNA
NM_021197	Homo sapiens WAP four-disulfide core domain 1 (WFDC1), mRNA
NM_007128	Homo sapiens pre-B lymphocyte gene 1 (VPREB1), mRNA
NM_006373	Homo sapiens vesicle amine transport protein 1 (VATI), mRNA
NM_003105	Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA
NM_020777	Homo sapiens VPS10 domain receptor protein (SORCS2), mRNA
NM_052918	Homo sapiens VPS10 domain receptor protein SORCS 1 (SORCS1), mRNA
NM_022553	Homo sapiens SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 2, mRNA
NM_004843	Homo sapiens class I cytokine receptor (WSX1), mRNA
NM_080564	Homo sapiens SAC2 suppressor of actin mutations 2-like (yeast) (SACM2L), transcript variant 1, mRNA
NM_006711	Homo sapiens RNA binding protein S1, serine-rich domain (RNPS1), transcript variant 1, mRNA
NM_080594	Homo sapiens RNA binding protein S1, serine-rich domain (RNPS1), transcript variant 2, mRNA
NM_100486	Homo sapiens WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 3, mRNA
NM_100264	Homo sapiens WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 2, mRNA
NM_016628	Homo sapiens WW domain-containing adapter with a coiled-coil region (WAC), transcript variant 1, mRNA

NM_005701	Homo sapiens RNA, U transporter 1 (RNUT1), mRNA
NM_014810	Homo sapiens centrosome-associated protein 350 (CAP350), mRNA
NM_013325	Homo sapiens KIAA0943 protein (Apg4B), mRNA
NM_020235	Homo sapiens bobby sox homolog (Drosophila) (BBX), mRNA
NM_019118	Homo sapiens hypothetical protein RP4-622L5 (RP4-622L5), mRNA
NM_016312	Homo sapiens WW domain binding protein 11 (WBP11), mRNA
NM_018706	Homo sapiens KIAA1630 protein (KIAA1630), mRNA
NM_080599	Homo sapiens regulator of nonsense transcripts 2 (RENT2), transcript variant 1, mRNA
NM_015542	Homo sapiens regulator of nonsense transcripts 2 (RENT2), transcript variant 2, mRNA
NM_002911	Homo sapiens regulator of nonsense transcripts 1 (RENT1), mRNA
NM_002833	Homo sapiens protein tyrosine phosphatase, non-receptor type 9 (PTPN9), mRNA
NM_080589	Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 3, mRNA
NM_080588	Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 2, mRNA
NM_002832	Homo sapiens protein tyrosine phosphatase, non-receptor type 7 (PTPN7), transcript variant 1, mRNA
NM_007039	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
NM_014369	Homo sapiens protein tyrosine phosphatase, non-receptor type 18 (brain-derived) (PTPN18), mRNA
NM_005401	Homo sapiens protein tyrosine phosphatase, non-receptor type 14 (PTPN14), mRNA
NM_002835	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
NM_080685	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 4, mRNA
NM_080684	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 3, mRNA
NM_080683	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 1, mRNA
NM_080601	Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (PTPN11), transcript variant 2, mRNA
NM_002834	Homo sapiens protein tyrosine phosphatase, non-receptor type 11 (PTPN11), transcript variant 1, mRNA
NM_006399	Homo sapiens basic leucine zipper transcription factor, ATF-like (BATF), mRNA
NM_006709	Homo sapiens HLA-B associated transcript 8 (BAT8), transcript variant NG36/G9a, mRNA
NM_033177	Homo sapiens HLA-B associated transcript 4 (BAT4), mRNA
NM_004639	Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 1, mRNA
NM_080703	Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 3, mRNA
NM_080702	Homo sapiens HLA-B associated transcript 3 (BAT3), transcript variant 2, mRNA
NM_004638	Homo sapiens HLA-B associated transcript 2 (BAT2), transcript variant 2, mRNA
NM_080686	Homo sapiens HLA-B associated transcript 2 (BAT2), transcript variant 1,

	mRNA
NM_004640	Homo sapiens HLA-B associated transcript 1 (BAT1), transcript variant 1, mRNA
NM_080598	Homo sapiens HLA-B associated transcript 1 (BAT1), transcript variant 2, mRNA
NM_080797	Homo sapiens death associated transcription factor 1 (DATF1), transcript variant 3, mRNA
NM_080796	Homo sapiens death associated transcription factor 1 (DATF1), transcript variant 2, mRNA
NM_022105	Homo sapiens death associated transcription factor 1 (DATF1), transcript variant 1, mRNA
NM_021080	Homo sapiens disabled homolog 1 (Drosophila) (DAB1), mRNA
NM_080760	Homo sapiens dachshund homolog (Drosophila) (DACH), transcript variant 2, mRNA
NM_080759	Homo sapiens dachshund homolog (Drosophila) (DACH), transcript variant 1, mRNA
NM_004392	Homo sapiens dachshund homolog (Drosophila) (DACH), transcript variant 3, mRNA
NM_005996	Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 1, mRNA
NM_016569	Homo sapiens T-box 3 (ulnar mammary syndrome) (TBX3), transcript variant 2, mRNA
NM_016954	Homo sapiens T-box 22 (TBX22), mRNA
NM_080701	Homo sapiens three prime repair exonuclease 2 (TREX2), transcript variant 4, mRNA
NM_080700	Homo sapiens three prime repair exonuclease 2 (TREX2), transcript variant 3, mRNA
NM_080699	Homo sapiens three prime repair exonuclease 2 (TREX2), transcript variant 2, mRNA
NM_017518	Homo sapiens three prime repair exonuclease 2 (TREX2), transcript variant 5, mRNA
NM_007205	Homo sapiens three prime repair exonuclease 2 (TREX2), transcript variant 1, mRNA
NM_080632	Homo sapiens similar to yeast Upf3, variant B (UPF3B), transcript variant 1, mRNA
NM_023010	Homo sapiens similar to yeast Upf3, variant B (UPF3B), transcript variant 2, mRNA
NM_080687	Homo sapiens similar to yeast Upf3, variant A (UPF3A), transcript variant 2, mRNA
NM_023011	Homo sapiens similar to yeast Upf3, variant A (UPF3A), transcript variant 1, mRNA
NM_080630	Homo sapiens collagen, type XI, alpha 1 (COL11A1), transcript variant C, mRNA
NM_080629	Homo sapiens collagen, type XI, alpha 1 (COL11A1), transcript variant B, mRNA
NM_001854	Homo sapiens collagen, type XI, alpha 1 (COL11A1), transcript variant A, mRNA
NM_080791	Homo sapiens acid phosphatase, testicular (ACPT), transcript variant A3, mRNA
NM_001639	Homo sapiens amyloid P component, serum (APCS), mRNA
NM_080790	Homo sapiens acid phosphatase, testicular (ACPT), transcript variant A2, mRNA
NM_080789	Homo sapiens acid phosphatase, testicular (ACPT), transcript variant A1, mRNA
NM_033068	Homo sapiens acid phosphatase, testicular (ACPT), transcript variant A, mRNA

NM_001649	Homo sapiens apical protein-like (Xenopus laevis) (APXL), mRNA
NM_014481	Homo sapiens apurinic/apyrimidinic endonuclease-like 2 (APEXL2), nuclear gene encoding mitochondrial protein, mRNA
NM_080649	Homo sapiens APEX nuclease (multifunctional DNA repair enzyme) (APEX), transcript variant 3, mRNA
NM_080648	Homo sapiens APEX nuclease (multifunctional DNA repair enzyme) (APEX), transcript variant 2, mRNA
NM_001641	Homo sapiens APEX nuclease (multifunctional DNA repair enzyme) (APEX), transcript variant 1, mRNA
NM_080839	Homo sapiens similar to gamma-glutamyltransferase 1 (LOC91227), mRNA
NM_080927	Homo sapiens endothelial and smooth muscle cell-derived neuropilin-like protein (ESDN), mRNA
NM_030969	Homo sapiens hypothetical protein MGC1223 (MGC1223), mRNA
NM_080920	Homo sapiens gamma-glutamyltransferase-like activity 4 (GGTLA4), mRNA
NM_021168	Homo sapiens RAR (RAS like GTPASE) like (RARL), mRNA
NM_080842	Homo sapiens hypothetical gene similar to gamma-glutamyltransferase-like activity 1 (LOC129026), mRNA
NM_031460	Homo sapiens potassium channel, subfamily K, member 17 (TASK-4) (KCNK17), mRNA
NM_033056	Homo sapiens protocadherin 15 (PCDH15), mRNA
NM_053283	Homo sapiens dermcidin (DCD), mRNA
NM_033518	Homo sapiens solute carrier family 38, member 5 (SLC38A5), mRNA
NM_021160	Homo sapiens HLA-B associated transcript 5 (BAT5), mRNA
NM_002279	Homo sapiens keratin, hair, acidic, 3B (KRTHA3B), mRNA
NM_004138	Homo sapiens keratin, hair, acidic, 3A (KRTHA3A), mRNA
NM_016310	Homo sapiens polymerase (RNA) III (DNA directed) polypeptide K (12.3 kD) (POLR3K), mRNA
NM_031991	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 3, mRNA
NM_031990	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 2, mRNA
NM_002819	Homo sapiens polypyrimidine tract binding protein 1 (PTBP1), transcript variant 1, mRNA
NM_030930	Homo sapiens unc-93 homolog B1 (C. elegans) (UNC93B1), mRNA
NM_022454	Homo sapiens SRY-related HMG-box transcription factor SOX17 (SOX17), mRNA
NM_004652	Homo sapiens ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 1, mRNA
NM_021906	Homo sapiens ubiquitin specific protease 9, X chromosome (fat facets-like Drosophila) (USP9X), transcript variant 2, mRNA
NM_022349	Homo sapiens membrane-spanning 4-domains, subfamily A, member 6A (MS4A6A), mRNA
NM_022122	Homo sapiens matrix metalloproteinase 27 (MMP27), mRNA
NM_006387	Homo sapiens calcium homeostasis endoplasmic reticulum protein (CHERP), mRNA
NM_006918	Homo sapiens sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, fungal)-like (SC5DL), mRNA
NM_020151	Homo sapiens START domain containing 7 (STARD7), mRNA
NM_018976	Homo sapiens solute carrier family 38, member 2 (SLC38A2), mRNA
NM_013351	Homo sapiens T-box 21 (TBX21), mRNA
NM_006993	Homo sapiens nucleophosmin/nucleoplasmin, 3 (NPM3), mRNA
NM_002420	Homo sapiens transient receptor potential cation channel, subfamily M, member

	1 (TRPM1), mRNA
NM_007244	Homo sapiens proline rich 4 (lacrimal) (PROL4), mRNA
NM_006758	Homo sapiens U2(RNU2) small nuclear RNA auxillary factor 1 (U2AF1), mRNA
NM_006264	Homo sapiens protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), transcript variant 2, mRNA
NM_006055	Homo sapiens LanC lantibiotic synthetase component C-like 1 (bacterial) (LANCL1), mRNA
NM_005716	Homo sapiens regulator of G-protein signalling 19 interacting protein 1 (RGS19IP1), mRNA
NM_005149	Homo sapiens T-box 19 (TBX19), mRNA
NM_004231	Homo sapiens ATPase, vacuolar, 14 kD (ATP6S14), mRNA
NM_000275	Homo sapiens oculocutaneous albinism II (pink-eye dilution homolog, mouse) (OCA2), mRNA
NM_001384	Homo sapiens diptheria toxin resistance protein required for diphthamide biosynthesis-like 2 (S. cerevisiae) (DPH2L2), mRNA
NM_000062	Homo sapiens serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary) (SERPING1), mRNA
NM_003307	Homo sapiens transient receptor potential cation channel, subfamily M, member 2 (TRPM2), mRNA
NM_003807	Homo sapiens tumor necrosis factor (ligand) superfamily, member 14 (TNFSF14), mRNA
NM_002984	Homo sapiens small inducible cytokine A4 (SCYA4), mRNA
NM_002105	Homo sapiens H2A histone family, member X (H2AFX), mRNA
NM_005331	Homo sapiens hemoglobin, theta 1 (HBQ1), mRNA
NM_000558	Homo sapiens hemoglobin, alpha 1 (HBA1), mRNA
NM_000517	Homo sapiens hemoglobin, alpha 2 (HBA2), mRNA
NM_012262	Homo sapiens heparan sulfate 2-O-sulfotransferase 1 (HS2ST1), mRNA
NM_021213	Homo sapiens phosphatidylcholine transfer protein (PCTP), mRNA
NM_018960	Homo sapiens glycine N-methyltransferase (GNMT), mRNA
NM_017807	Homo sapiens O-sialoglycoprotein endopeptidase (OSGEP), mRNA
NM_016732	Homo sapiens RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) (RALY), transcript variant 1, mRNA
NM_014483	Homo sapiens RNA binding motif, single stranded interacting protein (RBMS3), mRNA
NM_012320	Homo sapiens lysophospholipase 3 (LYPLA3), mRNA
NM_000184	Homo sapiens hemoglobin, gamma G (HBG2), mRNA
NM_005330	Homo sapiens hemoglobin, epsilon 1 (HBE1), mRNA
NM_007367	Homo sapiens RNA binding protein (autoantigenic, hnRNP-associated with lethal yellow) (RALY), transcript variant 2, mRNA
NM_005332	Homo sapiens hemoglobin, zeta (HBZ), mRNA
NM_005438	Homo sapiens FOS-like antigen 1 (FOSL1), mRNA
NM_000158	Homo sapiens glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type IV) (GBE1), mRNA
NM_000559	Homo sapiens hemoglobin, gamma A (HBG1), mRNA
NG_000007	Homo sapiens genomic beta globin region (HBB@) on chromosome 11
NG_000006	Homo sapiens genomic alpha globin region (HBA@) on chromosome 16
NM_030964	Homo sapiens sprouty homolog 4 (Drosophila) (SPRY4), mRNA
NM_021181	Homo sapiens 19A24 protein (CRACC), mRNA
NM_004654	Homo sapiens ubiquitin specific protease 9, Y chromosome (fat facets-like Drosophila) (USP9Y), mRNA
NM_018518	Homo sapiens MCM10 minichromosome maintenance deficient 10 (S.

	cerevisiae) (MCM10), mRNA
NM_018593	Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 10 (SLC16A10), mRNA
NM_018240	Homo sapiens kin of IRRE like (Drosophila) (KIRREL), mRNA
NM_016004	Homo sapiens chromosome 20 open reading frame 9 (C20orf9), mRNA
NM_006841	Homo sapiens solute carrier family 38, member 3 (SLC38A3), mRNA
NM_003725	Homo sapiens oxidative 3 alpha hydroxysteroid dehydrogenase; retinol dehydrogenase; 3-hydroxysteroid epimerase (RODH), mRNA
NG_000009	Homo sapiens genomic small histone family cluster (HFS@) on chromosome 6
NM_080878	Homo sapiens endothelial lectin HL-2 (HL-2), mRNA
NM_080876	Homo sapiens protein phosphatase (SKRP1), mRNA
NM_080874	Homo sapiens ankyrin repeat and SOCS box-containing 5 (ASB5), mRNA
NM_080873	Homo sapiens ankyrin repeat and SOCS box-containing 11 (ASB11), mRNA
NM_080872	Homo sapiens KIAA1777 protein (Unc5h4), mRNA
NM_080867	Homo sapiens suppressor of cytokine signalling 4 (SOCS4), mRNA
NM_080864	Homo sapiens relaxin 3 (H3) (RLN3), mRNA
NM_080863	Homo sapiens ankyrin repeat and SOCS box-containing 16 (ASB16), mRNA
NM_080862	Homo sapiens SPRY domain-containing SOCS box protein SSB-4 (SSB-4), mRNA
NM_080861	Homo sapiens SPRY domain-containing SOCS box protein SSB-3 (SSB-3), mRNA
NM_080860	Homo sapiens testes specific A2 homolog (mouse) (TSGA2), mRNA
NM_016150	Homo sapiens ankyrin repeat and SOCS box-containing 2 (ASB2), mRNA
NM_016127	Homo sapiens hypothetical protein MGC8721 (MGC8721), mRNA
NM_004170	Homo sapiens solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 (SLC1A1), nuclear gene encoding mitochondrial protein, mRNA
NM_017611	Homo sapiens hypothetical protein DKFZp762A227 (DKFZp762A227), mRNA
NM_025220	Homo sapiens a disintegrin and metalloproteinase domain 33 (ADAM33), mRNA
NM_018548	Homo sapiens down-regulated in lung cancer (HLCDGP1), mRNA
NM_080740	Homo sapiens similar to Ovis aries Y chromosome repeat region OY11.1 (3'OY11.1), mRNA
NM_012163	Homo sapiens F-box and leucine-rich repeat protein 9 (FBXL9), mRNA
NM_012304	Homo sapiens F-box and leucine-rich repeat protein 7 (FBXL7), mRNA
NM_012160	Homo sapiens F-box and leucine-rich repeat protein 4 (FBXL4), mRNA
NM_012159	Homo sapiens F-box and leucine-rich repeat protein 3B (FBXL3B), mRNA
NM_012158	Homo sapiens F-box and leucine-rich repeat protein 3A (FBXL3A), mRNA
NM_012157	Homo sapiens F-box and leucine-rich repeat protein 2 (FBXL2), mRNA
NM_024555	Homo sapiens F-box and leucine-rich repeat protein 6 (FBXL6), transcript variant 2, mRNA
NM_012162	Homo sapiens F-box and leucine-rich repeat protein 6 (FBXL6), transcript variant 1, mRNA
NM_033535	Homo sapiens F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 2, mRNA
NM_012161	Homo sapiens F-box and leucine-rich repeat protein 5 (FBXL5), transcript variant 1, mRNA
NM_002278	Homo sapiens keratin, hair, acidic, 2 (KRTHA2), mRNA
NM_033285	Homo sapiens tumor protein p53 inducible nuclear protein 1 (TP53INP1), mRNA
NM_002277	Homo sapiens keratin, hair, acidic, 1 (KRTHA1), mRNA
NM_032994	Homo sapiens Williams Beuren syndrome chromosome region 14 (WBSCR14),

	transcript variant 5, mRNA
NM_032954	Homo sapiens Williams Beuren syndrome chromosome region 14 (WBSCR14), transcript variant 4, mRNA
NM_032953	Homo sapiens Williams Beuren syndrome chromosome region 14 (WBSCR14), transcript variant 3, mRNA
NM_032952	Homo sapiens Williams Beuren syndrome chromosome region 14 (WBSCR14), transcript variant 2, mRNA
NM_032951	Homo sapiens Williams Beuren syndrome chromosome region 14 (WBSCR14), transcript variant 1, mRNA
NG_000008	Homo sapiens genomic cytochrome P450, subfamily IIA (phenobarbital-inducible) (CYP2A) on chromosome 19
NM_030809	Homo sapiens chromosome 12 open reading frame 22 (C12orf22), mRNA
NM_004426	Homo sapiens early development regulator 1 (polyhomeotic 1 homolog) (EDR1), mRNA
NM_020244	Homo sapiens choline phosphotransferase 1 (CHPT1), mRNA
NM_019074	Homo sapiens delta-like 4 (Drosophila) (DLL4), mRNA
NM_018990	Homo sapiens chromosome X open reading frame 9 (CXorf9), mRNA
NM_017833	Homo sapiens chromosome 21 open reading frame 55 (C21orf55), mRNA
NM_018255	Homo sapiens elongator protein 2 (ELP2), mRNA
NM_014096	Homo sapiens hypothetical protein DKFZp762A227 (DKFZp762A227), mRNA
NM_014927	Homo sapiens connector enhancer of KSR2 (CNK2), mRNA
NM_012164	Homo sapiens F-box and WD-40 domain protein 2 (FBXW2), mRNA
NM_012247	Homo sapiens selenium donor protein (SPS), mRNA
NM_012165	Homo sapiens F-box and WD-40 domain protein 3 (FBXW3), mRNA
NM_007198	Homo sapiens proline synthetase co-transcribed homolog (bacterial) (PROSC), mRNA
NM_006011	Homo sapiens sialyltransferase 8B (alpha-2, 8-sialytransferase) (SIAT8B), mRNA
NM_005674	Homo sapiens zinc finger protein 239 (ZNF239), mRNA
NM_001364	Homo sapiens discs, large homolog 2, chapsyn-110 (Drosophila) (DLG2), mRNA
NM_000646	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 6, mRNA
NM_000645	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 5, mRNA
NM_000644	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 2, mRNA
NM_000643	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 3, mRNA
NM_000642	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 1, mRNA
NM_000028	Homo sapiens amylo-1, 6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), transcript variant 4, mRNA
NM_080831	Homo sapiens chromosome 20 open reading frame 87 (C20orf87), mRNA
NM_080825	Homo sapiens chromosome 20 open reading frame 144 (C20orf144), mRNA
NM_080823	Homo sapiens chromosome 20 open reading frame 148 (C20orf148), mRNA

NM_017662	Homo sapiens transient receptor potential cation channel, subfamily M, member 6 (TRPM6), mRNA
NM_080744	Homo sapiens scavenger receptor cysteine rich domain containing, group B (4 domains) (SRCRB4D), mRNA
NM_000493	Homo sapiens collagen, type X, alpha 1(Schmid metaphyseal chondrodysplasia) (COL10A1), mRNA
NM_057096	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43), transcript variant 3, mRNA
NM_014578	Homo sapiens ras homolog gene family, member D (ARHD), mRNA
NM_020708	Homo sapiens solute carrier family 12, (potassium-chloride transporter) member 5 (SLC12A5), mRNA
NM_016093	Homo sapiens ribosomal protein L26-like 1 (RPL26L1), mRNA
NM_057095	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43), transcript variant 2, mRNA
NM_022820	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43), transcript variant 1, mRNA
NM_052969	Homo sapiens ribosomal protein L39-like (RPL39L), mRNA
NM_052970	Homo sapiens chromosome 20 open reading frame 60 (C20orf60), mRNA
NM_052865	Homo sapiens chromosome 20 open reading frame 72 (C20orf72), mRNA
NM_021029	Homo sapiens ribosomal protein L36a (RPL36A), mRNA
NM_001001	Homo sapiens ribosomal protein L36a-like (RPL36AL), mRNA
NM_033645	Homo sapiens F-box and WD-40 domain protein 1B (FBXW1B), transcript variant 1, mRNA
NM_033644	Homo sapiens F-box and WD-40 domain protein 1B (FBXW1B), transcript variant 2, mRNA
NM_012300	Homo sapiens F-box and WD-40 domain protein 1B (FBXW1B), transcript variant 3, mRNA
NM_022760	Homo sapiens chromosome 20 open reading frame 81 (C20orf81), mRNA
NM_014958	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 15 (ARHGEF15), mRNA
NM_021810	Homo sapiens cadherin-like 26 (CDH26), mRNA
NM_030876	Homo sapiens olfactory receptor, family 5, subfamily V, member 1 (OR5V1), mRNA
NM_031232	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein (APBA2BP), transcript variant 2, mRNA
NM_031231	Homo sapiens amyloid beta (A4) precursor protein-binding, family A, member 2 binding protein (APBA2BP), transcript variant 1, mRNA
NM_032554	Homo sapiens G protein-coupled receptor 81 (GPR81), mRNA
NM_006462	Homo sapiens chromosome 20 open reading frame 18 (C20orf18), transcript variant 1, mRNA
NM_031229	Homo sapiens chromosome 20 open reading frame 18 (C20orf18), transcript variant 2, mRNA
NM_031228	Homo sapiens chromosome 20 open reading frame 18 (C20orf18), transcript variant 3, mRNA
NM_031227	Homo sapiens chromosome 20 open reading frame 18 (C20orf18), transcript variant 4, mRNA
NM_031424	Homo sapiens chromosome 20 open reading frame 55 (C20orf55), mRNA
NM_000518	Homo sapiens hemoglobin, beta (HBB), mRNA
NM_030959	Homo sapiens olfactory receptor, family 12, subfamily D, member 3 (OR12D3), mRNA
NM_018661	Homo sapiens defensin, beta 3 (DEFB3), mRNA
NM_022487	Homo sapiens DNA cross-link repair 1C (PSO2 homolog, S. cerevisiae)

	(DCLRE1C), mRNA
NM_022099	Homo sapiens chromosome 20 open reading frame 51 (C20orf51), mRNA
NM_000668	Homo sapiens alcohol dehydrogenase IB (class I), beta polypeptide (ADH1B), mRNA
NM_021943	Homo sapiens testis expressed sequence 27 (TEX27), mRNA
NM_021640	Homo sapiens chromosome 12 open reading frame 10 (C12orf10), mRNA
NM_021215	Homo sapiens chromosome 20 open reading frame 77 (C20orf77), mRNA
NM_012141	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26 (DDX26), mRNA
NM_021225	Homo sapiens proline-rich 1 (PROL1), mRNA
NM_006508	Homo sapiens regenerating islet-derived-like, pancreatic stone protein-like, pancreatic thread protein-like (rat) (REGL), mRNA
NM_020356	Homo sapiens chromosome 20 open reading frame 32 (C20orf32), mRNA
NM_020369	Homo sapiens fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus) (FSCN3), mRNA
NM_020145	Homo sapiens SH3-domain GRB2-like endophilin B2 (SH3GLB2), mRNA
NM_020125	Homo sapiens BCM-like membrane protein precursor (BLAME), mRNA
NM_019025	Homo sapiens chromosome 20 open reading frame 16 (C20orf16), mRNA
NM_018679	Homo sapiens t-complex 11 (mouse) (TCP11), mRNA
NM_017589	Homo sapiens B-cell translocation gene 4 (BTG4), mRNA
NM_018692	Homo sapiens chromosome 20 open reading frame 17 (C20orf17), mRNA
NM_018697	Homo sapiens LanC lantibiotic synthetase component C-like 2 (bacterial) (LANCL2), mRNA
NM_018677	Homo sapiens acetyl-Coenzyme A synthetase 2 (ADP forming) (ACAS2), mRNA
NM_018431	Homo sapiens chromosome 20 open reading frame 180 (C20orf180), mRNA
NM_018725	Homo sapiens interleukin 17B receptor (IL17BR), mRNA
NM_018474	Homo sapiens chromosome 20 open reading frame 19 (C20orf19), mRNA
NM_018478	Homo sapiens chromosome 20 open reading frame 35 (C20orf35), mRNA
NM_017896	Homo sapiens chromosome 20 open reading frame 11 (C20orf11), mRNA
NM_017874	Homo sapiens chromosome 20 open reading frame 27 (C20orf27), mRNA
NM_017859	Homo sapiens uridine kinase-like 1 (URKL1), mRNA
NM_017798	Homo sapiens chromosome 20 open reading frame 21 (C20orf21), mRNA
NM_017789	Homo sapiens sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C (SEMA4C), mRNA
NM_017714	Homo sapiens chromosome 20 open reading frame 13 (C20orf13), mRNA
NM_017671	Homo sapiens chromosome 20 open reading frame 42 (C20orf42), mRNA
NM_018384	Homo sapiens immune associated nucleotide 4 like 1 (mouse) (IAN4L1), mRNA
NM_018354	Homo sapiens chromosome 20 open reading frame 46 (C20orf46), mRNA
NM_018347	Homo sapiens chromosome 20 open reading frame 29 (C20orf29), mRNA
NM_018327	Homo sapiens chromosome 20 open reading frame 38 (C20orf38), mRNA
NM_018282	Homo sapiens paraspeckle protein 1 (PSP1), mRNA
NM_018270	Homo sapiens chromosome 20 open reading frame 20 (C20orf20), mRNA
NM_018257	Homo sapiens chromosome 20 open reading frame 36 (C20orf36), mRNA
NM_018197	Homo sapiens zinc finger protein 64 homolog (mouse) (ZFP64), mRNA
NM_018010	Homo sapiens estrogen-related receptor beta like 1 (ESRRBL1), mRNA
NM_017446	Homo sapiens mitochondrial ribosomal protein L39 (MRPL39), mRNA
NM_017429	Homo sapiens beta-carotene 15, 15'-dioxygenase (BCDO), mRNA
NM_016082	Homo sapiens chromosome 20 open reading frame 34 (C20orf34), mRNA
NM_016610	Homo sapiens toll-like receptor 8 (TLR8), mRNA
NM_016009	Homo sapiens SH3-domain GRB2-like endophilin B1 (SH3GLB1), mRNA

NM_016408	Homo sapiens chromosome 20 open reading frame 34 (C20orf34), mRNA
NM_016407	Homo sapiens chromosome 20 open reading frame 43 (C20orf43), mRNA
NM_016319	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis) (COPS7A), mRNA
NM_015985	Homo sapiens angiopoietin 4 (ANGPT4), mRNA
NM_015834	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2c, mRNA
NM_015833	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRABA2b, mRNA
NM_014036	Homo sapiens BCM-like membrane protein precursor (BLAME), mRNA
NM_014012	Homo sapiens RAS (RAD and GEM)-like GTP-binding (REM), mRNA
NM_014841	Homo sapiens synaptosomal-associated protein, 91 kD homolog (mouse) (SNAP91), mRNA
NM_014795	Homo sapiens zinc finger homeobox 1b (ZFHX1B), mRNA
NM_015313	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 12 (ARHGEF12), mRNA
NM_014784	Homo sapiens Rho guanine nucleotide exchange factor (GEF) 11 (ARHGEF11), mRNA
NM_014862	Homo sapiens aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2), mRNA
NM_014054	Homo sapiens chromosome 20 open reading frame 40 (C20orf40), mRNA
NM_015629	Homo sapiens PRP31 pre-mRNA processing factor 31 homolog (yeast) (PRPF31), mRNA
NM_015417	Homo sapiens chromosome 20 open reading frame 28 (C20orf28), mRNA
NM_014625	Homo sapiens nephrosis 2, idiopathic, steroid-resistant (podocin) (NPHS2), mRNA
NM_014592	Homo sapiens Kv channel interacting protein 1 (KCNIP1), mRNA
NM_014140	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1 (SMARCAL1), mRNA
NM_013442	Homo sapiens stomatin (EPB72)-like 2 (STOML2), mRNA
NM_013248	Homo sapiens NUTF-like export factor1 (NXT1), mRNA
NM_013316	Homo sapiens CCR4-NOT transcription complex, subunit (CNOT4), mRNA
NM_013348	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 14 (KCNJ14), mRNA
NM_013279	Homo sapiens chromosome 11 open reading frame 9 (C11orf9), mRNA
NM_012418	Homo sapiens fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus) (FSCN2), mRNA
NM_012201	Homo sapiens golgi apparatus protein 1 (GLG1), mRNA
NM_000519	Homo sapiens hemoglobin, delta (HBD), mRNA
NM_006999	Homo sapiens polymerase (DNA directed) sigma (POLS), mRNA
NM_006719	Homo sapiens actin binding LIM protein (ABLIM), transcript variant ABLIM-m, mRNA
NM_002313	Homo sapiens actin binding LIM protein (ABLIM), transcript variant ABLIM-l, mRNA
NM_007238	Homo sapiens peroxisomal membrane protein 4 (24kD) (PXMP4), mRNA
NM_007184	Homo sapiens nischarin (NISCH), mRNA
NM_006720	Homo sapiens actin binding LIM protein (ABLIM), transcript variant ABLIM-s, mRNA
NM_007026	Homo sapiens dual specificity phosphatase 14 (DUSP14), mRNA
NM_006837	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 5 (Arabidopsis) (COPS5), mRNA
NM_006614	Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog

	of L1) (CHL1), mRNA
NM_006410	Homo sapiens HIV-1 Tat interactive protein 2, 30 kD (HTATIP2), mRNA
NM_006432	Homo sapiens Niemann-Pick disease, type C2 (NPC2), mRNA
NM_006348	Homo sapiens golgi transport complex 1 (90 kD subunit) (GOLTC1), mRNA
NM_006408	Homo sapiens anterior gradient 2 homolog (Xenepus laevis) (AGR2), mRNA
NM_006106	Homo sapiens Yes-associated protein 1, 65 kD (YAP1), mRNA
NM_006096	Homo sapiens N-myc downstream regulated gene 1 (NDRG1), mRNA
NM_006071	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly homolog, sea urchin)-like (PKDREJ), mRNA
NM_006092	Homo sapiens caspase recruitment domain family, member 4 (CARD4), mRNA
NM_005748	Homo sapiens YY1 associated factor 2 (YAF2), mRNA
NM_005715	Homo sapiens uronyl-2-sulfotransferase (UST), mRNA
NM_005622	Homo sapiens SA hypertension-associated homolog (rat) (SAH), mRNA
NM_005733	Homo sapiens RAB6 interacting, kinesin-like (rabkinesin6) (RAB6KIFL), mRNA
NM_005668	Homo sapiens sialyltransferase 8D (alpha-2, 8-polysialytransferase) (SIAT8D), mRNA
NM_005606	Homo sapiens legumain (LGMN), mRNA
NM_004649	Homo sapiens chromosome 21 open reading frame 33 (C21orf33), mRNA
NM_005469	Homo sapiens peroxisomal acyl-CoA thioesterase (PTE1), mRNA
NM_005180	Homo sapiens B lymphoma Mo-MLV insertion region (mouse) (BMI1), mRNA
NM_005108	Homo sapiens xylulokinase homolog (H. influenzae) (XYLB), mRNA
NM_004610	Homo sapiens t-complex 10 (mouse) (TCP10), mRNA
NM_004579	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 2 (MAP4K2), mRNA
NM_004086	Homo sapiens coagulation factor C homolog, cochlin (Limulus polyphemus) (COCH), mRNA
NM_004273	Homo sapiens carbohydrate (chondroitin 6) sulfotransferase 3 (CHST3), mRNA
NM_004902	Homo sapiens RNA-binding region (RNP1, RRM) containing 2 (RNPC2), mRNA
NM_004353	Homo sapiens serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1) (SERPINH1), mRNA
NM_004317	Homo sapiens arsA arsenite transporter, ATP-binding, homolog 1 (bacterial) (ASNA1), mRNA
NM_001247	Homo sapiens ectonucleoside triphosphate diphosphohydrolase 6 (putative function) (ENTPD6), mRNA
NM_003831	Homo sapiens sudD suppressor of bimD6 homolog (A. nidulans) (SUDD), mRNA
NM_003143	Homo sapiens single-stranded DNA binding protein (SSBP1), mRNA
NM_003098	Homo sapiens syntrophin, alpha 1 (dystrophin-associated protein A1, 59kD, acidic component) (SNTA1), mRNA
NM_003034	Homo sapiens sialyltransferase 8A (alpha-N-acetylneuraminate/alpha-2,8-sialytransferase, GD3 synthase) (SIAT8A), mRNA
NM_003028	Homo sapiens SHB (Src homology 2 domain-containing) adaptor protein B (SHB), mRNA
NM_003579	Homo sapiens RAD54-like (S. cerevisiae) (RAD54L), mRNA
NM_002669	Homo sapiens pleiotropic regulator 1 (PRL1homolog, Arabidopsis) (PLRG1), mRNA
NM_000139	Homo sapiens membrane-spanning 4-domains, subfamily A, member 1 (MS4A2), mRNA
NM_003836	Homo sapiens delta-like 1 homolog (Drosophila) (DLK1), mRNA
NM_003653	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 3

	(Arabidopsis) (COPS3), mRNA
NM_000083	Homo sapiens chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant) (CLCN1), mRNA
NM_000691	Homo sapiens aldehyde dehydrogenase 3 family, memberA1 (ALDH3A1), mRNA
NM_001112	Homo sapiens adenosine deaminase, RNA-specific, B1 (RED1 homolog rat) (ADARB1), transcript variant DRADA2a, mRNA
NM_004370	Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant long, mRNA
NM_080645	Homo sapiens collagen, type XII, alpha 1 (COL12A1), transcript variant short, mRNA
NM_080681	Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 2, mRNA
NM_080680	Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 1, mRNA
NM_080679	Homo sapiens collagen, type XI, alpha 2 (COL11A2), transcript variant 3, mRNA
NM_003593	Homo sapiens winged-helix nude (WHN), mRNA
NM_000638	Homo sapiens vitronectin (serum spreading factor, somatomedin B, complement S-protein) (VTN), mRNA
NM_080682	Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 2, mRNA
NM_001078	Homo sapiens vascular cell adhesion molecule 1 (VCAM1), transcript variant 1, mRNA
NM_006115	Homo sapiens preferentially expressed antigen in melanoma (PRAME), mRNA
NM_000175	Homo sapiens glucose phosphate isomerase (GPI), mRNA
NM_020526	Homo sapiens EphA8 (EPHA8), mRNA
NM_002109	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
NM_012208	Homo sapiens histidyl-tRNA synthetase-like (HARSL), mRNA
NM_004608	Homo sapiens T-box 6 (TBX6), transcript variant 1, mRNA
NM_080758	Homo sapiens T-box 6 (TBX6), transcript variant 2, mRNA
NM_080718	Homo sapiens T-box 5 (TBX5), transcript variant 2, mRNA
NM_080717	Homo sapiens T-box 5 (TBX5), transcript variant 3, mRNA
NM_000192	Homo sapiens T-box 5 (TBX5), transcript variant 1, mRNA
NM_080832	Homo sapiens poly(A) binding protein, cytoplasmic 5 (PABPC5), mRNA
NM_080824	Homo sapiens chromosome 20 open reading frame 106 (C20orf106), mRNA
NM_080822	Homo sapiens candidate tumor suppressor OVCA2 (OVCA2), mRNA
NM_080821	Homo sapiens chromosome 20 open reading frame 108 (C20orf108), mRNA
NM_080820	Homo sapiens chromosome 20 open reading frame 88 (C20orf88), mRNA
NM_080818	Homo sapiens G protein-coupled receptor 80 (GPR80), mRNA
NM_080817	Homo sapiens G protein-coupled receptor 82 (GPR82), mRNA
NM_080794	Homo sapiens mitochondrial ribosomal protein L39 (MRPL39), mRNA
NM_020973	Homo sapiens cytosolic beta-glucosidase (GLUC), mRNA
NM_054112	Homo sapiens chromosome 20 open reading frame 63 (C20orf63), mRNA
NM_052951	Homo sapiens chromosome 20 open reading frame 167 (C20orf167), mRNA
NM_014145	Homo sapiens chromosome 20 open reading frame 30 (C20orf30), mRNA
NM_033409	Homo sapiens chromosome 20 open reading frame 54 (C20orf54), mRNA
NM_032013	Homo sapiens NDRG family member 3 (NDRG3), mRNA
NM_032109	Homo sapiens orthopedia homolog (Drosophila) (OTP), mRNA
NM_024021	Homo sapiens membrane-spanning 4-domains, subfamily A, member 4 (MS4A4A), mRNA
NM_022910	Homo sapiens NDRG family member 4 (NDRG4), mRNA

NM_025206	Homo sapiens fer-1-like 4 (C. elegans) (FER1L4), mRNA
NM_024960	Homo sapiens chromosome 20 open reading frame 48 (C20orf48), mRNA
NM_024893	Homo sapiens chromosome 20 open reading frame 39 (C20orf39), mRNA
NM_024299	Homo sapiens chromosome 20 open reading frame 149 (C20orf149), mRNA
NM_024077	Homo sapiens SECIS binding protein 2 (SBP2), mRNA
NM_022730	Homo sapiens COP9 constitutive photomorphogenic homolog subunit 7B (Arabidopsis) (COPS7B), mRNA
NM_022574	Homo sapiens postmeiotic segregation increased 2-like 12 (PERQ1), mRNA
NM_022568	Homo sapiens aldehyde dehyrdogenase 8 family, member A1 (ALDH8A1), mRNA
NM_022477	Homo sapiens NDRG family member 3 (NDRG3), mRNA
NM_022082	Homo sapiens chromosome 20 open reading frame 59 (C20orf59), mRNA
NM_022058	Homo sapiens solute carrier family 4, sodium bicarbonate transporter-like, member 10 (SLC4A10), mRNA
NM_021230	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia3 (MLL3), mRNA
NM_021145	Homo sapiens cyclin D binding myb-like transcription factor 1 (DMTF1), mRNA
NM_005238	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA
NM_020465	Homo sapiens NDRG family member 4 (NDRG4), mRNA
NM_014227	Homo sapiens solute carrier family 5 (low affinity glucose cotransporter), member 4 (SLC5A4), mRNA
NM_015317	Homo sapiens pumilio homolog 2 (Drosophila) (PUM2), mRNA
NM_015665	Homo sapiens achalasia, adrenocortical insufficiency, alacrimia (Allgrove, triple-A) (AAAS), mRNA
NM_021950	Homo sapiens membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) (MS4A1), mRNA
NM_005589	Homo sapiens aldehyde dehydrogenase 6 family, member A1 (ALDH6A1), mRNA
NM_000533	Homo sapiens proteolipid protein1 (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated) (PLP1), mRNA
NM_016252	Homo sapiens baculoviral IAP repeat-containing 6 (apollon) (BIRC6), mRNA
NM_014351	Homo sapiens sulfotransferase family 4A, member 1 (SULT4A1), mRNA
NM_012323	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) (MAFF), mRNA
NM_006600	Homo sapiens nuclear distribution gene C homolog (A. nidulans) (NUDC), mRNA
NM_006145	Homo sapiens DnaJ (Hsp40) homolog, subfmaily B, member 1 (DNAJB1), mRNA
NM_005120	Homo sapiens trinucleotide repeat containing 11 (THR-associated protein, 230 kD subunit) (TNRC11), mRNA
NM_001383	Homo sapiens diptheria toxin resistance protein required for diphthamide biosynthesis-like 1 (S. cerevisiae) (DPH2L1), mRNA
NM_001327	Homo sapiens cancer/testis antigen 1 (CTAG1), mRNA
NM_080750	Homo sapiens chromosome 20 open reading frame 143 (C20orf143), mRNA
NM_032819	Homo sapiens zinc finger protein 341 (ZNF341), mRNA
NM_017895	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 27 (DDX27), mRNA
NM_030782	Homo sapiens cisplatin resistance related protein CRR9p (CRR9), mRNA
NM_080748	Homo sapiens chromosome 20 open reading frame 52 (C20orf52), mRNA
NM_080743	Homo sapiens serine-arginine repressor protein (35 kDa) (SRrp35), mRNA
NM_080742	Homo sapiens UDP-glucuronyltransferase-S (GLCATS), mRNA

NM_080741	Homo sapiens sialidase 4 (NEU4), mRNA
NM_080739	Homo sapiens chromosome 20 open reading frame 141 (C20orf141), mRNA
NM_033550	Homo sapiens chromosome 20 open reading frame 64 (C20orf64), mRNA
NM_080732	Homo sapiens egl nine homolog 2 (C. elegans) (EGLN2), transcript variant 3, mRNA
NM_053046	Homo sapiens egl nine homolog 2 (C. elegans) (EGLN2), transcript variant 1, mRNA
NM_025106	Homo sapiens SPRY domain-containing SOCS box protein SSB-1 (FLJ22393), mRNA
NM_030760	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA
NM_016069	Homo sapiens mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction (Magmas), nuclear gene encoding mitochondrial protein, mRNA
NM_021205	Homo sapiens Wnt-1 responsive Cdc42 homolog (WRCH-1), mRNA
NM_032495	Homo sapiens hypothetical protein SMAP31 (SMAP31), mRNA
NM_032556	Homo sapiens interleukin-1 HY2 (IL1HY2), mRNA
NM_014331	Homo sapiens solute carrier family 7, (cationic amino acid transporter, y+ system) member 11 (SLC7A11), mRNA
NM_017564	Homo sapiens stabilin-2 (STAB2), mRNA
NM_020924	Homo sapiens bioref (bioref), mRNA
NM_015356	Homo sapiens scribble (SCRIB), mRNA
NM_030648	Homo sapiens SET domain-containing protein 7 (SET7), mRNA
NM_018488	Homo sapiens T-box 4 (TBX4), mRNA
NM_016470	Homo sapiens chromosome 20 map 20q13.11
NM_080722	Homo sapiens a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 14 (ADAMTS14), mRNA
NM_080676	Homo sapiens chromosome 20 open reading frame 133 (C20orf133), mRNA
NM_080674	Homo sapiens chromosome 20 open reading frame 86 (C20orf86), mRNA
NM_080621	Homo sapiens chromosome 20 open reading frame 136 (C20orf136), mRNA
NM_080608	Homo sapiens chromosome 20 open reading frame 165 (C20orf165), mRNA
NM_080719	Homo sapiens hypothetical protein MGC4473 (MGC4473), mRNA
NM_003495	Homo sapiens H4 histone family, member M (H4FM), mRNA
NM_020633	Homo sapiens V1R-like 1 (V1RL1), mRNA
NM_007259	Homo sapiens vacuolar protein sorting 45A (yeast) (VPS45A), mRNA
NM_080631	Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 2, mRNA
NM_014396	Homo sapiens vacuolar protein sorting 41 (yeast) (VPS41), transcript variant 1, mRNA
NM_018668	Homo sapiens vacuolar protein sorting 33B (yeast) (VPS33B), mRNA
NM_022916	Homo sapiens vacuolar protein sorting 33A (rat homolog) (VPS33A), mRNA
NM_003610	Homo sapiens RAE1 RNA export 1 homolog (S. pombe) (RAE1), mRNA
NM_014061	Homo sapiens APR-1 protein (MAGEH1), mRNA
NM_001927	Homo sapiens desmin (DES), mRNA
NM_080593	Homo sapiens histone family member (H2B/S), mRNA
NM_080596	Homo sapiens histone family member (H2A/S), mRNA
NM_001867	Homo sapiens cytochrome c oxidase subunit VIIc (COX7C), nuclear gene encoding mitochondrial protein, mRNA
NM_001866	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA
NM_004718	Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 2 like (COX7A2L), nuclear gene encoding mitochondrial protein, mRNA

NM_001865	Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 2 (liver) (COX7A2), nuclear gene encoding mitochondrial protein, mRNA
NM_001864	Homo sapiens cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA
NM_006438	Homo sapiens collectin sub-family member 10 (C-type lectin) (COLEC10), mRNA
NM_080544	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant VIII, mRNA
NM_080543	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant VII, mRNA
NM_080542	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant VI, mRNA
NM_080541	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant V, mRNA
NM_080540	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant IV, mRNA
NM_080539	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant III, mRNA
NM_080538	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant II, mRNA
NM_005677	Homo sapiens collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholinesterase (COLQ), transcript variant I, mRNA
NM_080592	Homo sapiens apoptosis related protein APR-3 (APR-3), transcript variant 2, mRNA
NM_016085	Homo sapiens apoptosis related protein APR-3 (APR-3), transcript variant 1, mRNA
NM_014318	Homo sapiens apoptosis related protein (APR-2), mRNA
NM_001745	Homo sapiens calcium modulating ligand (CAMLG), mRNA
NM_004341	Homo sapiens carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase (CAD),, nuclear gene encoding mitochondrial protein, mRNA
NM_032493	Homo sapiens adaptor-related protein complex 1, mu 1 subunit (AP1M1), mRNA
NM_001128	Homo sapiens adaptor-related protein complex 1, gamma 1 subunit (AP1G1), mRNA
NM_080545	Homo sapiens adaptor-related protein complex 1, gamma 2 subunit (AP1G2), transcript variant 2, mRNA
NM_003917	Homo sapiens adaptor-related protein complex 1, gamma 2 subunit (AP1G2), transcript variant 1, mRNA
NM_080549	Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6), transcript variant 3, mRNA
NM_080548	Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6), transcript variant 2, mRNA
NM_002831	Homo sapiens protein tyrosine phosphatase, non-receptor type 6 (PTPN6), transcript variant 1, mRNA
NM_002830	Homo sapiens protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte) (PTPN4), mRNA
NM_002829	Homo sapiens protein tyrosine phosphatase, non-receptor type 3 (PTPN3), mRNA
NM_080423	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 3, mRNA
NM_080422	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2),

	transcript variant 2, mRNA
NM_002828	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2), transcript variant 1, mRNA
NM_002827	Homo sapiens protein tyrosine phosphatase, non-receptor type 1 (PTPN1), mRNA
NM_014241	Homo sapiens protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a (PTPLA), mRNA
NM_003479	Homo sapiens protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 1, mRNA
NM_080392	Homo sapiens protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 3, mRNA
NM_080391	Homo sapiens protein tyrosine phosphatase type IVA, member 2 (PTP4A2), transcript variant 2, mRNA
NM_080591	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 2, mRNA
NM_000962	Homo sapiens prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1), transcript variant 1, mRNA
NM_004058	Homo sapiens calcyphosine (CAPS), transcript variant 1, mRNA
NM_080590	Homo sapiens calcyphosine (CAPS), transcript variant 2, mRNA
NM_006380	Homo sapiens amyloid beta precursor protein (cytoplasmic tail) binding protein 2 (APPBP2), mRNA
NM_003905	Homo sapiens amyloid beta precursor protein binding protein 1, 59kD (APPBP1), mRNA
NM_005783	Homo sapiens ATP binding protein associated with cell differentiation (APACD), mRNA
NM_080600	Homo sapiens myelin associated glycoprotein (MAG), transcript variant 2, mRNA
NM_002361	Homo sapiens myelin associated glycoprotein (MAG), transcript variant 1, mRNA
NM_005994	Homo sapiens T-box 2 (TBX2), mRNA
NM_080647	Homo sapiens T-box 1 (TBX1), transcript variant C, mRNA
NM_080646	Homo sapiens T-box 1 (TBX1), transcript variant A, mRNA
NM_080675	Homo sapiens sperm associated antigen 4-like (SPAG4L), mRNA
NM_080617	Homo sapiens cerebellin precursor-like 1 (CBLNL1), mRNA
NM_080611	Homo sapiens dual specificity phosphatase-like 15 (DUSP15), mRNA
NM_080610	Homo sapiens cystatin 9-like (mouse) (CST9L), mRNA
NM_080602	Homo sapiens actin related protein 2/3 complex, subunit 3B (21 kD) (ARPC3B), mRNA
NG_000011	Homo sapiens genomic cytochrome P450, subfamily IIA (phenobarbital-inducible) (CYP2A.3@) on chromosome 19
NM_016649	Homo sapiens chromosome 20 open reading frame 6 (C20orf6), mRNA
NM_080597	Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), mRNA
NM_080605	Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 6 (B3GALT6), mRNA
NM_058169	Homo sapiens loss of heterozygosity, 12, chromosomal region 1 (LOH12CR1), mRNA
NM_058164	Homo sapiens olfactomedin 2 (OLFM2), mRNA
NM_052866	Homo sapiens ADAMTS-like 1 (ADAMTSL1), mRNA
NM_018030	Homo sapiens oxysterol binding protein-like 1A (OSBPL1A), mRNA
NM_033142	Homo sapiens chorionic gonadotropin, beta polypeptide 7 (CGB7), mRNA
NG_000013	Homo sapiens genomic MHC class III complement gene cluster (MCGC@) on chromosome 6

NM_020967	Homo sapiens nuclear receptor coactivator 5 (NCOA5), mRNA
NM_033044	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 3, mRNA
NM_033024	Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant 2, mRNA
NG_000017	Homo sapiens genomic protocadherin beta cluster (PCDHB@) on chromosome 5
NM_015864	Homo sapiens chromosome 6 open reading frame 32 (C6orf32), mRNA
NM_032188	Homo sapiens histone acetyltransferase MYST1 (MYST1), mRNA
NM_030776	Homo sapiens chromosome 20 open reading frame 183 (C20orf183), mRNA
NM_024918	Homo sapiens chromosome 20 open reading frame 172 (C20orf172), mRNA
NM_024812	Homo sapiens brain and acute leukemia, cytoplasmic (BAALC), mRNA
NM_024777	Homo sapiens chromosome 20 open reading frame 124 (C20orf124), mRNA
NM_024758	Homo sapiens agmatinase (FLJ23384), mRNA
NM_024641	Homo sapiens mandaselin (FLJ12838), mRNA
NM_024331	Homo sapiens chromosome 20 open reading frame 121 (C20orf121), mRNA
NM_024301	Homo sapiens fukutin-related protein (FKRP), mRNA
NM_005763	Homo sapiens aminoadipate-semialdehyde synthase (AASS), mRNA
NM_023935	Homo sapiens chromosome 20 open reading frame 116 (C20orf116), mRNA
NM_021993	Homo sapiens FUS interacting protein (serine-arginine rich) 2 (FUSIP2), mRNA
NM_014555	Homo sapiens transient receptor potential cation channel, subfamily M, member 5 (TRPM5), mRNA
NM_000537	Homo sapiens renin (REN), mRNA
NM_016652	Homo sapiens Crn, crooked neck-like 1 (Drosophila) (CRNKL1), mRNA
NM_021245	Homo sapiens myozenin 1 (MYOZ1), mRNA
NM_001967	Homo sapiens eukaryotic translation initiation factor 4A, isoform 2 (EIF4A2), mRNA
NM_018649	Homo sapiens H2A histone family, member Y2 (H2AFY2), mRNA
NM_015148	Homo sapiens PAS domain containing serine/threonine kinase (PASK), mRNA
NM_017902	Homo sapiens hypoxia-inducible factor 1, alpha subunit inhibitor (HIF1AN), mRNA
NM_018285	Homo sapiens chromosome 15 open reading frame 12 (C15orf12), nuclear gene encoding mitochondrial protein, mRNA
NM_018267	Homo sapiens H2A histone family, member J (H2AFJ), mRNA
NM_017555	Homo sapiens egl nine homolog 2 (C. elegans) (EGLN2), transcript variant 2, mRNA
NM_016143	Homo sapiens likely ortholog of rat p47 (p47), mRNA
NM_015993	Homo sapiens plasmolipin (PMLP), mRNA
NM_014938	Homo sapiens Mlx interactor (MONDOA), mRNA
NM_014948	Homo sapiens likely ortholog of mouse ubiquitin conjugating enzyme 7 interacting protein 5 (UBCE7IP5), mRNA
NM_014016	Homo sapiens SAC1 suppressor of actin mutations 1-like (yeast) (SACM1L), mRNA
NM_015156	Homo sapiens REST corepressor (RCOR), mRNA
NM_013337	Homo sapiens translocase of inner mitochondrial membrane 22 homolog (yeast) (TIMM22), mRNA
NM_013233	Homo sapiens serine threonine kinase 39 (STE20/SPS1 homolog, yeast) (STK39), mRNA
NM_006595	Homo sapiens apoptosis inhibitor 5 (API5), mRNA
NM_006402	Homo sapiens hepatitis B virus x interacting protein (HBXIP), mRNA
NM_006351	Homo sapiens translocase of inner mitochondrial membrane 44 homolog (yeast) (TIMM44), mRNA
NM_006327	Homo sapiens translocase of inner mitochondrial membrane 23 homolog (yeast)

	(TIMM23), mRNA
NM_006335	Homo sapiens translocase of inner mitochondrial membrane 17 homolog A (yeast) (TIMM17A), mRNA
NM_006420	Homo sapiens ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibited) (ARFGEF2), mRNA
NM_005992	Homo sapiens T-box 1 (TBX1), transcript variant B, mRNA
NM_005834	Homo sapiens translocase of inner mitochondrial membrane 17 homolog B (yeast) (TIMM17B), mRNA
NM_000385	Homo sapiens aquaporin 1 (channel-forming integral protein, 28kD) (AQP1), mRNA
NM_002891	Homo sapiens Ras protein-specific guanine nucleotide-releasing factor 1 (RASGRF1), mRNA
NM_000963	Homo sapiens prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2), mRNA
NM_002792	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7), mRNA
NM_002335	Homo sapiens low density lipoprotein receptor-related protein 5 (LRP5), mRNA
NM_001402	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
NM_080677	Homo sapiens dynein light chain 2 (Dlc2), mRNA
NM_080672	Homo sapiens Q9H4T4 like (H17739), mRNA
NM_080671	Homo sapiens potassium voltage-gated channel, Isk-related subfamily, gene 4 (KCNE4), mRNA
NM_080670	Homo sapiens similar to RIKEN cDNA 2610030J16 gene (MGC2541), mRNA
NM_080669	Homo sapiens similar to RIKEN cDNA 1110002C08 gene (MGC9564), mRNA
NM_080667	Homo sapiens similar to RIKEN cDNA 4931428D14 gene (MGC15407), mRNA
NM_080665	Homo sapiens similar to RIKEN cDNA B230118G17 gene (MGC19604), mRNA
NM_080664	Homo sapiens similar to RIKEN cDNA 4930578F06 gene (MGC9912), mRNA
NM_080662	Homo sapiens similar to RIKEN cDNA 1810022F11 gene (MGC4281), mRNA
NM_080660	Homo sapiens similar to RIKEN cDNA 1200014N16 gene (MGC14289), mRNA
NM_080659	Homo sapiens similar to RIKEN cDNA 2310030G06 gene (MGC14839), mRNA
NM_080657	Homo sapiens vipirin (cig5), mRNA
NM_080655	Homo sapiens similar to RIKEN cDNA 5730528L13 gene (MGC17337), mRNA
NM_080654	Homo sapiens NY-REN-41 antigen (NY-REN-41), mRNA
NM_080653	Homo sapiens similar to RIKEN cDNA 4930500C14 gene (MGC9341), mRNA
NM_080652	Homo sapiens similar to RIKEN cDNA 5730578N08 gene (MGC15397), mRNA
NM_004296	Homo sapiens regulator of G-protein signalling 6 (RGS6), mRNA
NM_014234	Homo sapiens FabG (beta-ketoacyl-[acyl-carrier-protein] reductase, E coli) like (E. coli) (FABGL), mRNA
NM_024775	Homo sapiens gemin 6 (GEMIN6), mRNA
NM_080626	Homo sapiens BRI3 binding protein (BRI3BP), mRNA
NM_080625	Homo sapiens chromosome 20 open reading frame 160 (C20orf160), mRNA
NM_080616	Homo sapiens chromosome 20 open reading frame 112 (C20orf112), mRNA
NM_080612	Homo sapiens DOS/Gab family member 3 (GAB3), mRNA
NM_080607	Homo sapiens chromosome 20 open reading frame 102 (C20orf102), mRNA
NM_080603	Homo sapiens chromosome 20 open reading frame 162 (C20orf162), mRNA
NM_032019	Homo sapiens histone deacetylase 10 (HDAC10), mRNA
NM_030815	Homo sapiens chromosome 20 open reading frame 126 (C20orf126), mRNA
NM_020841	Homo sapiens oxysterol binding protein-like 8 (OSBPL8), mRNA
NM_020764	Homo sapiens cask-interacting protein 1 (CASKIN1), mRNA
NM_016436	Homo sapiens chromosome 20 open reading frame 104 (C20orf104), mRNA

NM_022104	Homo sapiens chromosome 20 open reading frame 67 (C20orf67), mRNA
NM_080546	Homo sapiens CDw92 antigen (CDW92), mRNA
NM_015511	Homo sapiens chromosome 20 open reading frame 4 (C20orf4), mRNA
NM_002116	Homo sapiens major histocompatibility complex, class I, A (HLA-A), mRNA
NM_023017	Homo sapiens phosphoinositide 3-kinase enhancer (PIKE), mRNA
NM_020933	Homo sapiens zinc finger protein 317 (ZNF317), mRNA
NM_005037	Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), mRNA
NM_018206	Homo sapiens vacuolar protein sorting 35 (yeast) (VPS35), mRNA
NM_014003	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 38 (DDX38), mRNA
NM_006445	Homo sapiens PRP8 pre-mRNA processing factor 8 homolog (yeast) (PRPF8), mRNA
NM_003675	Homo sapiens pre-mRNA processing factor 18 (PRP18), mRNA
NM_006214	Homo sapiens phytanoyl-CoA hydroxylase (Refsum disease) (PHYH), mRNA
NM_004374	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
NM_001863	Homo sapiens cytochrome c oxidase subunit VIb (COX6B), nuclear gene encoding mitochondrial protein, mRNA
NM_005205	Homo sapiens cytochrome c oxidase subunit VIa polypeptide 2 (COX6A2), nuclear gene encoding mitochondrial protein, mRNA
NM_004373	Homo sapiens cytochrome c oxidase subunit VIa polypeptide 1 (COX6A1), nuclear gene encoding mitochondrial protein, mRNA
NM_032609	Homo sapiens cytochrome c oxidase subunit IV isoform 2 (COX4I2), nuclear gene encoding mitochondrial protein, mRNA
NM_032489	Homo sapiens acrosin binding protein (ACRBP), mRNA
NM_080476	Homo sapiens CDC91 cell division cycle 91-like 1 (S. cerevisiae) (CDC91L1), mRNA
NM_080473	Homo sapiens GATA binding protein 5 (GATA5), mRNA
NM_002121	Homo sapiens major histocompatibility complex, class II, DP beta 1 (HLA-DPB1), mRNA
NM_078470	Homo sapiens COX15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA
NM_004375	Homo sapiens COX11 homolog, cytochrome c oxidase assembly protein (yeast) (COX11), nuclear gene encoding mitochondrial protein, mRNA
NM_001303	Homo sapiens COX10 homolog, cytochrome c oxidase assembly protein, heme A/farnesyltransferase (yeast) (COX10), nuclear gene encoding mitochondrial protein, mRNA
NM_054028	Homo sapiens acyl-malonyl condensing enzyme (AMAC), mRNA
NM_032485	Homo sapiens chromosome 20 open reading frame 154 (C20orf154), mRNA
NM_033342	Homo sapiens tripartite motif-containing 7 (TRIM7), mRNA
NM_033421	Homo sapiens chromosome 20 open reading frame 161 (C20orf161), mRNA
NM_033197	Homo sapiens chromosome 20 open reading frame 114 (C20orf114), mRNA
NM_020866	Homo sapiens kelch-like 1 (Drosophila) (KLHL1), mRNA
NM_032883	Homo sapiens chromosome 20 open reading frame 100 (C20orf100), mRNA
NM_032523	Homo sapiens oxysterol binding protein-like 6 (OSBPL6), mRNA
NM_020896	Homo sapiens oxysterol binding protein-like 5 (OSBPL5), mRNA
NM_015550	Homo sapiens oxysterol binding protein-like 3 (OSBPL3), mRNA
NM_031473	Homo sapiens carnitine deficiency-associated gene expressed in ventricle 1 (CDV-1), mRNA
NM_030801	Homo sapiens MAGE-E1 protein (MAGE-E1), mRNA

NM_025128	Homo sapiens MUS81 endonuclease (MUS81), mRNA
NM_024958	Homo sapiens chromosome 20 open reading frame 98 (C20orf98), mRNA
NM_024663	Homo sapiens aminopeptidase-like 1 (NPEPL1), mRNA
NM_024586	Homo sapiens oxysterol binding protein-like 9 (OSBPL9), mRNA
NM_024120	Homo sapiens chromosome 20 open reading frame 7 (C20orf7), mRNA
NM_022776	Homo sapiens oxysterol binding protein-like 11 (OSBPL11), mRNA
NM_022109	Homo sapiens CDw92 antigen (CDW92), mRNA
NM_022088	Homo sapiens zinc finger protein 338 (ZNF338), mRNA
NM_021158	Homo sapiens chromosome 20 open reading frame 97 (C20orf97), mRNA
NM_021232	Homo sapiens proline dehydrogenase (oxidase) 2 (PRODH2), mRNA
NM_021220	Homo sapiens zinc finger protein 339 (ZNF339), mRNA
NM_021039	Homo sapiens S100 calcium binding protein A14 (calgizzarin) (S100A14), mRNA
NM_020659	Homo sapiens tweety homolog 1 (Drosophila) (TTYH1), mRNA
NM_018972	Homo sapiens ganglioside-induced differentiation-associated protein 1 (GDAP1), mRNA
NM_017921	Homo sapiens hypothetical protein FLJ20657 (NPL4), mRNA
NM_017784	Homo sapiens oxysterol binding protein-like 10 (OSBPL10), mRNA
NM_017731	Homo sapiens oxysterol binding protein-like 7 (OSBPL7), mRNA
NM_018209	Homo sapiens ADP-ribosylation factor 1 GTPase activating protein (ARF1GAP), mRNA
NM_018102	Homo sapiens zinc finger protein 334 (ZNF334), mRNA
NM_015891	Homo sapiens pre-mRNA splicing factor 17 (PRP17), mRNA
NM_016599	Homo sapiens myozenin 2 (MYOZ2), mRNA
NM_014962	Homo sapiens BTB (POZ) domain containing 3 (BTBD3), mRNA
NM_014835	Homo sapiens oxysterol binding protein-like 2 (OSBPL2), mRNA
NM_014723	Homo sapiens syntaphilin (SNPH), mRNA
NM_014183	Homo sapiens dynein light chain 2A (DNLC2A), mRNA
NM_014055	Homo sapiens carnitine deficiency-associated gene expressed in ventricle 1 (CDV-1), mRNA
NM_014477	Homo sapiens chromosome 20 open reading frame 10 (C20orf10), mRNA
NM_012261	Homo sapiens chromosome 20 open reading frame 103 (C20orf103), mRNA
NM_013369	Homo sapiens DNA (cytosine-5-)-methyltransferase 3-like (DNMT3L), mRNA
NM_012469	Homo sapiens chromosome 20 open reading frame 14 (C20orf14), mRNA
NM_012291	Homo sapiens extra spindle poles like 1 (S. cerevisiae) (ESPL1), mRNA
NM_007002	Homo sapiens adhesion regulating molecule 1 (ADRM1), mRNA
NM_006809	Homo sapiens translocase of outer mitochondrial membrane 34 (TOMM34), mRNA
NM_006813	Homo sapiens proline rich 2 (PROL2), mRNA
NM_002509	Homo sapiens NK2 transcription factor homolog B (Drosophila) (NKX2B), mRNA
NM_080474	Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12 (SERPINB12), mRNA
NM_006009	Homo sapiens tubulin, alpha 3 (TUBA3), mRNA
NM_003463	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA
NM_019888	Homo sapiens melanocortin 3 receptor (MC3R), mRNA
NM_001846	Homo sapiens collagen, type IV, alpha 2 (COL4A2), mRNA
NM_079422	Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), transcript variant 3f, mRNA
NM_079420	Homo sapiens myosin, light polypeptide 1, alkali; skeletal, fast (MYL1), transcript variant 1f, mRNA

NM_000795	Homo sapiens dopamine receptor D2 (DRD2), transcript variant 1, mRNA
NM_016574	Homo sapiens dopamine receptor D2 (DRD2), transcript variant 2, mRNA
NM_079837	Homo sapiens BTG3 associated nuclear protein (BANP), transcript variant 2, mRNA
NM_017869	Homo sapiens BTG3 associated nuclear protein (BANP), transcript variant 1, mRNA
NM_079425	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 3, mRNA
NM_079424	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 4, mRNA
NM_079423	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 2, mRNA
NM_021019	Homo sapiens myosin, light polypeptide 6, alkali, smooth muscle and non-muscle (MYL6), transcript variant 1, mRNA
NM_004509	Homo sapiens SP110 nuclear body protein (SP110), transcript variant a, mRNA
NM_080424	Homo sapiens SP110 nuclear body protein (SP110), transcript variant c, mRNA
NM_004510	Homo sapiens SP110 nuclear body protein (SP110), transcript variant b, mRNA
NM_004574	Homo sapiens peanut-like 2 (Drosophila) (PNUTL2), transcript variant 1, mRNA
NM_080417	Homo sapiens peanut-like 2 (Drosophila) (PNUTL2), transcript variant 4, mRNA
NM_080416	Homo sapiens peanut-like 2 (Drosophila) (PNUTL2), transcript variant 3, mRNA
NM_080415	Homo sapiens peanut-like 2 (Drosophila) (PNUTL2), transcript variant 2, mRNA
NM_002117	Homo sapiens major histocompatibility complex, class I, C (HLA-C), mRNA
NM_005514	Homo sapiens major histocompatibility complex, class I, B (HLA-B), mRNA
NC_001807	Homo sapiens mitochondrion, complete genome
NM_080489	Homo sapiens syndecan binding protein (syntenin) 2 (SDCBP2), mRNA
NM_001997	Homo sapiens Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived); ribosomal protein S30 (FAU), mRNA
NM_057179	Homo sapiens likely ortholog of mouse and rat twist-related bHLH protein Dermo-1 (DERMO1), mRNA
NM_001008	Homo sapiens ribosomal protein S4, Y-linked (RPS4Y), mRNA
NM_001007	Homo sapiens ribosomal protein S4, X-linked (RPS4X), mRNA
NM_005192	Homo sapiens cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase) (CDKN3), mRNA
NM_079421	Homo sapiens cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) (CDKN2D), transcript variant 2, mRNA
NM_001800	Homo sapiens cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4) (CDKN2D), transcript variant 1, mRNA
NM_078626	Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), transcript variant 2, mRNA
NM_001262	Homo sapiens cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (CDKN2C), transcript variant 1, mRNA
NM_078487	Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 2, mRNA
NM_004936	Homo sapiens cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (CDKN2B), transcript variant 1, mRNA
NM_004896	Homo sapiens vacuolar protein sorting 26 (yeast) (VPS26), mRNA
NM_052945	Homo sapiens BAFF receptor (BAFFR), mRNA
NM_022648	Homo sapiens tensin (TNS), mRNA
NM_078480	Homo sapiens fuse-binding protein-interacting repressor (SIAHBP1), transcript variant 1, mRNA
NM_014281	Homo sapiens fuse-binding protein-interacting repressor (SIAHBP1), transcript variant 2, mRNA

NM_004740	Homo sapiens TGFB1-induced anti-apoptotic factor 1 (TIAF1), transcript variant 2, mRNA
NM_078471	Homo sapiens TGFB1-induced anti-apoptotic factor 1 (TIAF1), transcript variant 1, mRNA
NM_001852	Homo sapiens collagen, type IX, alpha 2 (COL9A2), mRNA
NM_078485	Homo sapiens collagen, type IX, alpha 1 (COL9A1), transcript variant 2, mRNA
NM_001851	Homo sapiens collagen, type IX, alpha 1 (COL9A1), transcript variant 1, mRNA
NM_054026	Homo sapiens CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 2, mRNA
NM_013354	Homo sapiens CCR4-NOT transcription complex, subunit 7 (CNOT7), transcript variant 1, mRNA
NM_004064	Homo sapiens cyclin-dependent kinase inhibitor 1B (p27, Kip1) (CDKN1B), mRNA
NM_000389	Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 1, mRNA
NM_078467	Homo sapiens cyclin-dependent kinase inhibitor 1A (p21, Cip1) (CDKN1A), transcript variant 2, mRNA
NM_003936	Homo sapiens cyclin-dependent kinase 5, regulatory subunit 2 (p39) (CDK5R2), mRNA
NM_004642	Homo sapiens CDK2-associated protein 1 (CDK2AP1), mRNA
NM_078481	Homo sapiens CD97 antigen (CD97), transcript variant 1, mRNA
NM_001784	Homo sapiens CD97 antigen (CD97), transcript variant 2, mRNA
NM_080432	Homo sapiens vacuolar protein sorting protein 18 (VPS18), transcript variant 2, mRNA
NM_020857	Homo sapiens vacuolar protein sorting protein 18 (VPS18), transcript variant 1, mRNA
NM_080414	Homo sapiens vacuolar protein sorting 16 (yeast) (VPS16), transcript variant 2, mRNA
NM_080413	Homo sapiens vacuolar protein sorting 16 (yeast) (VPS16), transcript variant 3, mRNA
NM_022575	Homo sapiens vacuolar protein sorting 16 (yeast) (VPS16), transcript variant 1, mRNA
NM_021729	Homo sapiens vacuolar protein sorting 11 (yeast) (VPS11), mRNA
NM_005806	Homo sapiens oligodendrocyte lineage transcription factor 2 (OLIG2), mRNA
NM_012106	Homo sapiens binder of Arl Two (BART1), mRNA
NM_006095	Homo sapiens ATPase, aminophospholipid transporter (APLT), Class I, type 8A, member 1 (ATP8A1), mRNA
NM_058241	Homo sapiens cyclin T2 (CCNT2), transcript variant b, mRNA
NM_001241	Homo sapiens cyclin T2 (CCNT2), transcript variant a, mRNA
NM_001240	Homo sapiens cyclin T1 (CCNT1), mRNA
NM_000474	Homo sapiens twist homolog (acrocephalosyndactyly 3; Saethre-Chotzen syndrome) (Drosophila) (TWIST), mRNA
NM_080475	Homo sapiens serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 11 (SERPINB11), mRNA
NM_021209	Homo sapiens caspase recruitment domain protein 12 (CARD12), mRNA
NM_014550	Homo sapiens caspase recruitment domain protein 10 (CARD10), mRNA
NM_012287	Homo sapiens centaurin, beta 2 (CENTB2), mRNA
NM_007049	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 1, mRNA
NM_078476	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), transcript variant 2, mRNA
NM_004444	Homo sapiens EphB4 (EPHB4), mRNA

NM_004443	Homo sapiens EphB3 (EPHB3), mRNA
NM_004442	Homo sapiens EphB2 (EPHB2), transcript variant 1, mRNA
NM_017449	Homo sapiens EphB2 (EPHB2), transcript variant 2, mRNA
NM_004535	Homo sapiens myelin transcription factor 1 (MYT1), mRNA
NM_006800	Homo sapiens male-specific lethal 3-like 1 (Drosophila) (MSL3L1), transcript variant 3, mRNA
NM_078630	Homo sapiens male-specific lethal 3-like 1 (Drosophila) (MSL3L1), transcript variant 2, mRNA
NM_078629	Homo sapiens male-specific lethal 3-like 1 (Drosophila) (MSL3L1), transcript variant 1, mRNA
NM_078628	Homo sapiens male-specific lethal 3-like 1 (Drosophila) (MSL3L1), transcript variant 4, mRNA
NM_080431	Homo sapiens actin related protein M2 (ARPM2), mRNA
NM_080430	Homo sapiens selenoprotein SelM (SELM), mRNA
NM_052944	Homo sapiens putative sodium-coupled cotransporter RKST1 (RKST1), mRNA
NM_024831	Homo sapiens nuclear receptor coactivator 6 interacting protein (NCOA6IP), mRNA
NM_032803	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 3 (SLC7A3), mRNA
NM_080385	Homo sapiens carboxypeptidase A5 (CPA5), mRNA
NM_016476	Homo sapiens APC11 anaphase promoting complex subunit 11 homolog (yeast) (ANAPC11), mRNA
NM_080389	Homo sapiens defensin, beta 4 (DEFB4), mRNA
NM_032646	Homo sapiens tweety homolog 2 (Drosophila) (TTYH2), mRNA
NM_006928	Homo sapiens silver homolog (mouse) (SILV), mRNA
NM_080390	Homo sapiens my048 protein (my048), mRNA
NM_080388	Homo sapiens hypothetical protein MGC17528 (MGC17528), mRNA
NM_080387	Homo sapiens C-type lectin-like receptor (CLEC-6), mRNA
NM_080284	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 6 (ABCA6), mRNA
NM_080283	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 9 (ABCA9), mRNA
NM_080282	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 10 (ABCA10), mRNA
NM_006549	Homo sapiens calcium/calmodulin-dependent protein kinase kinase 2, beta (CAMKK2), mRNA
NM_007200	Homo sapiens A kinase (PRKA) anchor protein 13 (AKAP13), mRNA
NM_002476	Homo sapiens myosin, light polypeptide 4, alkali; atrial, embryonic (MYL4), mRNA
NM_001853	Homo sapiens collagen, type IX, alpha 3 (COL9A3), mRNA
NM_006001	Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 1, mRNA
NM_079836	Homo sapiens tubulin, alpha 2 (TUBA2), transcript variant 2, mRNA
NM_006000	Homo sapiens tubulin, alpha 1 (testis specific) (TUBA1), mRNA
NM_004376	Homo sapiens COX15 homolog, cytochrome c oxidase assembly protein (yeast) (COX15), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA
NM_024407	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 7 (20kD) (NADH-coenzyme Q reductase) (NDUFS7), mRNA
NM_078625	Homo sapiens vanin 3 (VNN3), transcript variant 2, mRNA
NM_018399	Homo sapiens vanin 3 (VNN3), transcript variant 1, mRNA
NM_078488	Homo sapiens vanin 2 (VNN2), transcript variant 2, mRNA
NM_004665	Homo sapiens vanin 2 (VNN2), transcript variant 1, mRNA

NM_013245	Homo sapiens vacuolar protein sorting factor 4A (VPS4A), mRNA
NM_058240	Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant b, mRNA
NM_033262	Homo sapiens solute carrier family 8 (sodium-calcium exchanger), member 3 (SLC8A3), transcript variant a, mRNA
NM_004869	Homo sapiens suppressor of K+ transport defect 1 (SKD1), mRNA
NM_078474	Homo sapiens BBP-like protein 2 (BLP2), transcript variant 1, mRNA
NM_025141	Homo sapiens BBP-like protein 2 (BLP2), transcript variant 2, mRNA
NM_078473	Homo sapiens BBP-like protein 1 (BLP1), transcript variant 1, mRNA
NM_031940	Homo sapiens BBP-like protein 1 (BLP1), transcript variant 2, mRNA
NM_020749	Homo sapiens AT2 receptor-interacting protein 1 (ATIP1), mRNA
NM_018672	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 5 (ABCA5), mRNA
NM_020177	Homo sapiens feminization 1 homolog a (FEM1A), mRNA
NM_002088	Homo sapiens glutamate receptor, ionotropic, kainate 5 (GRIK5), mRNA
NM_006835	Homo sapiens cyclin I (CCNI), mRNA
NM_001239	Homo sapiens cyclin H (CCNH), mRNA
NM_014286	Homo sapiens frequenin homolog (Drosophila) (FREQ), mRNA
NM_006650	Homo sapiens complexin 2 (CPLX2), mRNA
NM_006651	Homo sapiens complexin 1 (CPLX1), mRNA
NM_006463	Homo sapiens associated molecule with the SH3 domain of STAM (AMSH), mRNA
NM_001850	Homo sapiens collagen, type VIII, alpha 1 (COL8A1), mRNA
NM_000094	Homo sapiens collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive) (COL7A1), mRNA
NM_000077	Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 1, mRNA
NM_058197	Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 3, mRNA
NM_058196	Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 2, mRNA
NM_058195	Homo sapiens cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A), transcript variant 4, mRNA
NM_014800	Homo sapiens engulfment and cell motility 1 (ced-12 homolog, C. elegans) (ELMO1), mRNA
NM_079834	Homo sapiens secretory carrier membrane protein 4 (SCAMP-4), mRNA
NM_019110	Homo sapiens hypothetical protein P1 p373c6 (P1P373C6), mRNA
NM_022086	Homo sapiens engulfment and cell motility 2 (ced-12 homolog, C. elegans) (ELMO2), mRNA
NM_058183	Homo sapiens SON DNA binding protein (SON), mRNA
NM_003103	Homo sapiens SON DNA binding protein (SON), mRNA
NM_030767	Homo sapiens AT-hook transcription factor AKNA (AKNA), mRNA
NM_058191	Homo sapiens chromosome 21 open reading frame 66 (C21orf66), mRNA
NM_015657	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 12 (ABCA12), mRNA
NM_020427	Homo sapiens ARS component B (ARS), mRNA
NM_021638	Homo sapiens actin filament associated protein (AFAP), mRNA
NM_005782	Homo sapiens transcriptional coactivator (ALY), mRNA
NM_031916	Homo sapiens AKAP-associated sperm protein (ASP), mRNA
NM_024083	Homo sapiens alveolar soft part sarcoma chromosome region, candidate 1 (ASPSCR1), mRNA
NM_058230	Homo sapiens zinc finger protein 354B (ZNF354B), mRNA

NM_021935	Homo sapiens homolog of mouse Bv8 (Bombina variegata 8 kDa); prokineticin 2 precursor (BV8), mRNA
NM_015399	Homo sapiens breast cancer metastasis-suppressor 1 (BRMS1), mRNA
NM_007073	Homo sapiens blood vessel epicardial substance (BVES), mRNA
NM_017726	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 14D (PPP1R14D), mRNA
NM_006451	Homo sapiens polyadenylate binding protein-interacting protein 1 (PAIP1), mRNA
NM_018073	Homo sapiens SSA protein SS-56 (SS-56), mRNA
NM_032812	Homo sapiens tumor endothelial marker 7-related precursor (TEM7R), mRNA
NM_022748	Homo sapiens tumor endothelial marker 6 (TEM6), mRNA
NM_032777	Homo sapiens tumor endothelial marker 5 precursor (TEM5), mRNA
NM_022779	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31 (DDX31), mRNA
NM_018454	Homo sapiens nucleolar protein ANKT (ANKT), mRNA
NM_016489	Homo sapiens uridine 5' monophosphate hydrolase 1 (UMPH1), mRNA
NM_078483	Homo sapiens lysosomal amino acid transporter 1 (LYAAT1), mRNA
NM_019606	Homo sapiens hypothetical protein FLJ20257 (FLJ20257), mRNA
NM_015256	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 6 (FACL6), mRNA
NM_003393	Homo sapiens wingless-type MMTV integration site family, member 8B (WNT8B), mRNA
NM_058244	Homo sapiens wingless-type MMTV integration site family, member 8A (WNT8A), transcript variant 2, mRNA
NM_058238	Homo sapiens wingless-type MMTV integration site family, member 7B (WNT7B), mRNA
NM_004625	Homo sapiens wingless-type MMTV integration site family, member 7A (WNT7A), mRNA
NM_058242	Homo sapiens keratin 6C (KRT6C), mRNA
NM_005555	Homo sapiens keratin 6B (KRT6B), mRNA
NM_005554	Homo sapiens keratin 6A (KRT6A), mRNA
NM_058207	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant E, mRNA
NM_058206	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant B, mRNA
NM_058203	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant C, mRNA
NM_058202	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant H, mRNA
NM_058201	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant D, mRNA
NM_058200	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant G, mRNA
NM_016512	Homo sapiens sperm associated antigen 11 (SPAG11), transcript variant A, mRNA
NM_057180	Homo sapiens vacuolar protein sorting 29 (yeast) (VPS29), transcript variant 2, mRNA
NM_016226	Homo sapiens vacuolar protein sorting 29 (yeast) (VPS29), transcript variant 1, mRNA
NM_053004	Homo sapiens guanine nucleotide binding protein (G protein), beta polypeptide 1-like (GNB1L), mRNA
NM_003902	Homo sapiens far upstream element (FUSE) binding protein 1 (FUBP1), mRNA
NM_058217	Homo sapiens RAD51 homolog C (S. cerevisiae) (RAD51C), transcript variant

	3, mRNA
NM_058216	Homo sapiens RAD51 homolog C (S. cerevisiae) (RAD51C), transcript variant 1, mRNA
NM_002876	Homo sapiens RAD51 homolog C (S. cerevisiae) (RAD51C), transcript variant 2, mRNA
NM_058179	Homo sapiens phosphoserine aminotransferase (PSA), transcript variant 1, mRNA
NM_021154	Homo sapiens phosphoserine aminotransferase (PSA), transcript variant 2, mRNA
NM_078469	Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant C, mRNA
NM_078468	Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant B, mRNA
NM_016567	Homo sapiens BRCA2 and CDKN1A interacting protein (BCCIP), transcript variant A, mRNA
NM_058177	Homo sapiens histone deacetylase 9 (HDAC9-PENDING), transcript variant 2, mRNA
NM_058176	Homo sapiens histone deacetylase 9 (HDAC9-PENDING), transcript variant 1, mRNA
NM_022110	Homo sapiens FK506 binding protein like (FKBPL), mRNA
NM_012181	Homo sapiens FK506 binding protein 8 (38kD) (FKBP8), mRNA
NM_003602	Homo sapiens FK506 binding protein 6 (36kD) (FKBP6), mRNA
NM_004117	Homo sapiens FK506 binding protein 5 (FKBP5), mRNA
NM_002014	Homo sapiens FK506 binding protein 4 (59kD) (FKBP4), mRNA
NM_057092	Homo sapiens FK506 binding protein 2 (13kD) (FKBP2), transcript variant 2, mRNA
NM_004470	Homo sapiens FK506 binding protein 2 (13kD) (FKBP2), transcript variant 1, mRNA
NM_004116	Homo sapiens FK506 binding protein 1B (12.6 kD) (FKBP1B), transcript variant 1, mRNA
NM_054033	Homo sapiens FK506 binding protein 1B (12.6 kD) (FKBP1B), transcript variant 2, mRNA
NM_000801	Homo sapiens FK506 binding protein 1A (12kD) (FKBP1A), transcript variant 12B, mRNA
NM_054014	Homo sapiens FK506 binding protein 1A (12kD) (FKBP1A), transcript variant 12A, mRNA
NM_057175	Homo sapiens hypothetical protein FLJ13340 (FLJ13340), transcript variant 1, mRNA
NM_025085	Homo sapiens hypothetical protein FLJ13340 (FLJ13340), transcript variant 2, mRNA
NM_014708	Homo sapiens kinetochore associated 1 (KNTC1), mRNA
NM_058199	Homo sapiens olfactomedin 1 (OLFM1), transcript variant 3, mRNA
NM_014279	Homo sapiens olfactomedin 1 (OLFM1), transcript variant 1, mRNA
NM_057174	Homo sapiens peroxisomal biogenesis factor 16 (PEX16), transcript variant 2, mRNA
NM_033118	Homo sapiens myosin light chain kinase 2, skeletal muscle (MYLK2), mRNA
NM_019117	Homo sapiens kelch-like 4 (Drosophila) (KLHL4), transcript variant 1, mRNA
NM_005103	Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 1, mRNA
NM_022549	Homo sapiens fasciculation and elongation protein zeta 1 (zygin I) (FEZ1), transcript variant 2, mRNA
NM_005112	Homo sapiens WD repeat domain 1 (WDR1), transcript variant 2, mRNA

NM_017491	Homo sapiens WD repeat domain 1 (WDR1), transcript variant 1, mRNA
NM_001862	Homo sapiens cytochrome c oxidase subunit Vb (COX5B), nuclear gene encoding mitochondrial protein, mRNA
NM_004255	Homo sapiens cytochrome c oxidase subunit Va (COX5A), nuclear gene encoding mitochondrial protein, mRNA
NM_057162	Homo sapiens kelch-like 4 (Drosophila) (KLHL4), transcript variant 2, mRNA
NM_033427	Homo sapiens cortactin binding protein 2 (CORTBP2), mRNA
NM_001799	Homo sapiens cyclin-dependent kinase 7 (MO15 homolog, Xenopus laevis, cdk-activating kinase) (CDK7), mRNA
NM_057089	Homo sapiens adaptor-related protein complex 1, sigma 1 subunit (AP1S1), transcript variant 2, mRNA
NM_001283	Homo sapiens adaptor-related protein complex 1, sigma 1 subunit (AP1S1), transcript variant 1, mRNA
NM_005148	Homo sapiens unc-119 homolog (C. elegans) (UNC119), transcript variant 1, mRNA
NM_054035	Homo sapiens unc-119 homolog (C. elegans) (UNC119), transcript variant 2, mRNA
NM_017675	Homo sapiens protocadherin LKC (PC-LKC), mRNA
NM_002401	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA
NM_003728	Homo sapiens unc-5 homolog B (C. elegans) (UNC5C), mRNA
NM_004673	Homo sapiens angiopoietin-like 1 (ANGPTL1), mRNA
NM_054016	Homo sapiens FUS interacting protein (serine-arginine rich) 1 (FUSIP1), transcript variant 2, mRNA
NM_006625	Homo sapiens FUS interacting protein (serine-arginine rich) 1 (FUSIP1), transcript variant 1, mRNA
NM_054027	Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), transcript variant 2, mRNA
NM_019847	Homo sapiens ankylosis, progressive homolog (mouse) (ANKH), transcript variant 1, mRNA
NM_006363	Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcript variant 1, mRNA
NM_032986	Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcript variant 3, mRNA
NM_032985	Homo sapiens Sec23 homolog B (S. cerevisiae) (SEC23B), transcript variant 2, mRNA
NM_053285	Homo sapiens tektin 1 (TEKT1), mRNA
NM_018440	Homo sapiens phosphoprotein associated with glycosphingolipid-enriched microdomains (PAG), mRNA
NM_014479	Homo sapiens ADAM-like, decysin 1 (ADAMDEC1), mRNA
NM_016545	Homo sapiens immediate early response 5 (IER5), mRNA
NM_052820	Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 2, mRNA
NM_003389	Homo sapiens coronin, actin binding protein, 2A (CORO2A), transcript variant 1, mRNA
NM_032587	Homo sapiens caspase recruitment domain family, member 6 (CARD6), mRNA
NM_052814	Homo sapiens caspase recruitment domain family, member 9 (CARD9), transcript variant 2, mRNA
NM_052813	Homo sapiens caspase recruitment domain family, member 9 (CARD9), transcript variant 1, mRNA
NM_022352	Homo sapiens caspase recruitment domain family, member 9 (CARD9), transcript variant 3, mRNA

NM_052978	Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 2, mRNA
NM_015163	Homo sapiens tripartite motif-containing 9 (TRIM9), transcript variant 1, mRNA
NM_052840	Homo sapiens bruno-like 6, RNA binding protein (Drosophila) (BRUNOL6), mRNA
NM_000967	Homo sapiens ribosomal protein L3 (RPL3), mRNA
NM_015125	Homo sapiens capicua homolog (Drosophila) (CIC), mRNA
NM_018256	Homo sapiens WD repeat domain 12 (WDR12), mRNA
NM_016601	Homo sapiens potassium channel, subfamily K, member 9 (TASK-3) (KCNK9), mRNA
NM_033415	Homo sapiens hypothetical gene MGC19595 (MGC19595), mRNA
NM_001253	Homo sapiens CDC5 cell division cycle 5-like (S. pombe) (CDC5L), mRNA
NM_007065	Homo sapiens CDC37 cell division cycle 37 homolog (S. cerevisiae) (CDC37), mRNA
NM_003504	Homo sapiens CDC45 cell division cycle 45-like (S. cerevisiae) (CDC45L), mRNA
NM_006035	Homo sapiens CDC42 binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
NM_044472	Homo sapiens cell division cycle 42 (GTP binding protein, 25kD) (CDC42), transcript variant 2, mRNA
NM_001791	Homo sapiens cell division cycle 42 (GTP binding protein, 25kD) (CDC42), transcript variant 1, mRNA
NM_001254	Homo sapiens CDC6 cell division cycle 6 homolog (S. cerevisiae) (CDC6), mRNA
NM_022894	Homo sapiens poly(A) polymerase gamma (PAPOLG), mRNA
NM_033655	Homo sapiens cell recognition molecule CASPR3 (CASPR3), transcript variant 1, mRNA
NM_024879	Homo sapiens cell recognition molecule CASPR3 (CASPR3), transcript variant 2, mRNA
NM_012115	Homo sapiens CASP8 associated protein 2 (CASP8AP2), mRNA
NM_012173	Homo sapiens F-box only protein 25 (FBXO25), mRNA
NM_033624	Homo sapiens F-box only protein 21 (FBXO21), transcript variant 1, mRNA
NM_015002	Homo sapiens F-box only protein 21 (FBXO21), transcript variant 2, mRNA
NM_033625	Homo sapiens ribosomal protein L34 (RPL34), transcript variant 2, mRNA
NM_000995	Homo sapiens ribosomal protein L34 (RPL34), transcript variant 1, mRNA
NM_033540	Homo sapiens mitofusin 1 (MFN1), transcript variant 1, mRNA
NM_005612	Homo sapiens RE1-silencing transcription factor (REST), mRNA
NM_007085	Homo sapiens follistatin-like 1 (FSTL1), mRNA
NM_000993	Homo sapiens ribosomal protein L31 (RPL31), mRNA
NM_012180	Homo sapiens F-box only protein 8 (FBXO8), mRNA
NM_033182	Homo sapiens F-box protein FBX30 (FBX30), mRNA
NM_033406	Homo sapiens F-box only protein 3 (FBXO3), transcript variant 2, mRNA
NM_012175	Homo sapiens F-box only protein 3 (FBXO3), transcript variant 1, mRNA
NM_017425	Homo sapiens sperm autoantigenic protein 17 (SPA17), mRNA
NM_005633	Homo sapiens son of sevenless homolog 1 (Drosophila) (SOS1), mRNA
NM_003333	Homo sapiens ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52), mRNA
NM_019894	Homo sapiens transmembrane protease, serine 4 (TMPRSS4), mRNA
NM_033313	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 3, mRNA
NM_033312	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A), transcript variant 2, mRNA
NM_003672	Homo sapiens CDC14 cell division cycle 14 homolog A (S. cerevisiae)

	(CDC14A), transcript variant 1, mRNA
NM_005786	Homo sapiens serologically defined colon cancer antigen 33 (SDCCAG33), mRNA
NM_003618	Homo sapiens mitogen-activated protein kinase kinase kinase kinase 3 (MAP4K3), mRNA
NM_006577	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 (B3GNT1), transcript variant 1, mRNA
NM_020981	Homo sapiens UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1 (B3GALT1), mRNA
NM_033252	Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 (B3GNT1), transcript variant 2, mRNA
NM_002954	Homo sapiens ribosomal protein S27a (RPS27A), mRNA
NM_000971	Homo sapiens ribosomal protein L7 (RPL7), mRNA
NM_033344	Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA
NM_024023	Homo sapiens unkempt-like (Drosophila) (UNKL), mRNA
NM_033221	Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 4, mRNA
NM_033220	Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 3, mRNA
NM_033219	Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 2, mRNA
NM_014788	Homo sapiens tripartite motif-containing 14 (TRIM14), transcript variant 1, mRNA
NM_006074	Homo sapiens tripartite motif-containing 22 (TRIM22), mRNA
NM_012210	Homo sapiens tripartite motif-containing 32 (TRIM32), mRNA
NM_007276	Homo sapiens chromobox homolog 3 (HP1 gamma homolog, Drosophila) (CBX3), mRNA
NM_025227	Homo sapiens hypothetical protein dJ726C3.2 (DJ726C3.2), mRNA
NM_015271	Homo sapiens tripartite motif-containing 2 (TRIM2), mRNA
NM_017838	Homo sapiens nucleolar protein family A, member 2 (H/ACA small nucleolar RNPs) (NOLA2), mRNA
NM_032993	Homo sapiens nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) (NOLA1), transcript variant 2, mRNA
NM_018983	Homo sapiens nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs) (NOLA1), transcript variant 1, mRNA
NM_004722	Homo sapiens adaptor-related protein complex 4, mu 1 subunit (AP4M1), mRNA
NM_033066	Homo sapiens membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4) (MPP4), mRNA
NM_033030	Homo sapiens bol, boule-like (Drosophila) (BOLL), mRNA
NM_004216	Homo sapiens death effector domain-containing (DEDD), transcript variant 2, mRNA
NM_032998	Homo sapiens death effector domain-containing (DEDD), transcript variant 1, mRNA
NM_033010	Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 4, mRNA
NM_033009	Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 2, mRNA
NM_033008	Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 3, mRNA
NM_020418	Homo sapiens poly(rC) binding protein 4 (PCBP4), transcript variant 1, mRNA
NM_032944	Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 2, mRNA
NM_031414	Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA
NM_014302	Homo sapiens Sec61 gamma (SEC61G), mRNA
NM_013336	Homo sapiens protein transport protein SEC61 alpha subunit isoform 1

	(SEC61A1), mRNA
NM_031431	Homo sapiens tethering factor SEC34 (SEC34), mRNA
NM_015490	Homo sapiens secretory pathway component Sec31B-1 (SEC31B-1), mRNA
NM_004892	Homo sapiens SEC22 vesicle trafficking protein-like 1 (S. cerevisiae) (SEC22L1), mRNA
NM_032970	Homo sapiens vesicle trafficking protein (SEC22C), transcript variant 1, mRNA
NM_000969	Homo sapiens ribosomal protein L5 (RPL5), mRNA
NM_005034	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide K (7.0kD) (POLR2K), mRNA
NM_014459	Homo sapiens protocadherin 17 (PCDH17), mRNA
NM_032961	Homo sapiens protocadherin 10 (PCDH10), transcript variant 1, mRNA
NM_020815	Homo sapiens protocadherin 10 (PCDH10), transcript variant 2, mRNA
NM_031988	Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 2, mRNA
NM_002758	Homo sapiens mitogen-activated protein kinase kinase 6 (MAP2K6), transcript variant 1, mRNA
NM_032419	Homo sapiens dom-3 homolog Z (C. elegans) (DOM3Z), transcript variant 1, mRNA
NM_032966	Homo sapiens Burkitt lymphoma receptor 1, GTP binding protein (BLR1), transcript variant 2, mRNA
NM_001716	Homo sapiens Burkitt lymphoma receptor 1, GTP binding protein (BLR1), transcript variant 1, mRNA
NM_004951	Homo sapiens Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor) (EBI2), mRNA
NM_004874	Homo sapiens BCL2-associated athanogene 4 (BAG4), mRNA
NM_001016	Homo sapiens ribosomal protein S12 (RPS12), mRNA
NM_031994	Homo sapiens ring finger protein 17 (RNF17), transcript variant short, mRNA
NM_031271	Homo sapiens testis expressed sequence 15 (TEX15), mRNA
NM_018995	Homo sapiens Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse) (MOV10L1), mRNA
NM_032510	Homo sapiens par-6 partitioning defective 6 homolog gamma (C. elegans) (PARD6G), mRNA
NM_006704	Homo sapiens suppressor of G2 allele of SKP1, S. cerevisiae, homolog of (SGT1), mRNA
NM_031968	Homo sapiens nuclear prelamin A recognition factor (NARF), transcript variant 2, mRNA
NM_012336	Homo sapiens nuclear prelamin A recognition factor (NARF), transcript variant 1, mRNA
NM_003980	Homo sapiens microtubule-associated protein 7 (MAP7), mRNA
NM_032380	Homo sapiens elongation factor G2 (EFG2), mRNA
NM_032214	Homo sapiens Src-like-adaptor 2 (SLA2), mRNA
NM_020064	Homo sapiens BarH-like 1 (Drosophila) (BARHL1), mRNA
NM_005916	Homo sapiens MCM7 minichromosome maintenance deficient 7 (S. cerevisiae) (MCM7), mRNA
NM_004098	Homo sapiens empty spiracles homolog 2 (Drosophila) (EMX2), mRNA
NM_005826	Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA
NM_006418	Homo sapiens differentially expressed in hematopoietic lineages (GW112), mRNA
NM_005016	Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 1, mRNA
NM_031989	Homo sapiens poly(rC) binding protein 2 (PCBP2), transcript variant 2, mRNA
NM_006196	Homo sapiens poly(rC) binding protein 1 (PCBP1), mRNA
NM_031844	Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment

	factor A) (HNRPU), transcript variant 1, mRNA
NM_004501	Homo sapiens heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) (HNRPU), transcript variant 2, mRNA
NM_004500	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 2, mRNA
NM_031314	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC), transcript variant 1, mRNA
NM_031370	Homo sapiens heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD) (HNRPD), transcript variant 1, mRNA
NM_031369	Homo sapiens heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD) (HNRPD), transcript variant 2, mRNA
NM_002138	Homo sapiens heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kD) (HNRPD), transcript variant 3, mRNA
NM_003903	Homo sapiens CDC16 cell division cycle 16 homolog (S. cerevisiae) (CDC16), mRNA
NM_031483	Homo sapiens itchy homolog E3 ubiquitin protein ligase (mouse) (ITCH), mRNA
NM_031907	Homo sapiens ubiquitin specific protease 26 (USP26), mRNA
NM_031866	Homo sapiens frizzled homolog 8 (Drosophila) (FZD8), mRNA
NG_000004	Homo sapiens genomic cytochrome P450, subfamily IIIA (niphedipine oxidase) (CYP3A) on chromosome 7
NM_001788	Homo sapiens CDC10 cell division cycle 10 homolog (S. cerevisiae) (CDC10), mRNA
NM_004276	Homo sapiens calcium binding protein 1 (calbrain) (CABP1), transcript variant 2, mRNA
NM_031205	Homo sapiens calcium binding protein 1 (calbrain) (CABP1), transcript variant 1, mRNA
NM_000784	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1), nuclear gene encoding mitochondrial protein, mRNA
NM_031491	Homo sapiens retinol binding protein 5, cellular (RBP5), mRNA
NM_006929	Homo sapiens superkiller viralicidic activity 2-like (S. cerevisiae) (SKIV2L), mRNA
NM_001447	Homo sapiens FAT tumor suppressor homolog 2 (Drosophila) (FAT2), mRNA
NM_007242	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19 (DBP5 homolog, yeast) (DDX19), mRNA
NM_006773	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated) (DDX18), mRNA
NM_030655	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11), transcript variant 3, mRNA
NM_030653	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11), transcript variant 1, mRNA
NM_000770	Homo sapiens cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8 (CYP2C8), transcript variant Hp1-1, mRNA
NM_030878	Homo sapiens cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 8 (CYP2C8), transcript variant Hp1-2, mRNA
NM_012239	Homo sapiens sirtuin silent mating type information regulation 2 homolog 3 (S. cerevisiae) (SIRT3), mRNA
NM_030593	Homo sapiens sirtuin silent mating type information regulation 2 homolog 2 (S. cerevisiae) (SIRT2), transcript variant 2, mRNA
NM_012237	Homo sapiens sirtuin silent mating type information regulation 2 homolog 2 (S. cerevisiae) (SIRT2), transcript variant 1, mRNA

NM_012238	Homo sapiens sirtuin silent mating type information regulation 2 homolog 1 (S. cerevisiae) (SIRT1), mRNA
NM_031309	Homo sapiens scratch homolog 1, zinc finger protein (Drosophila) (SCRT1), mRNA
NM_031278	Homo sapiens tudor domain containing 1 (TDRD1), mRNA
NM_031277	Homo sapiens ring finger protein 17 (RNF17), transcript variant long, mRNA
NM_031276	Homo sapiens testis expressed sequence 11 (TEX11), mRNA
NM_031273	Homo sapiens testis expressed sequence 13B (TEX13B), mRNA
NM_031272	Homo sapiens testis expressed sequence 14 (TEX14), mRNA
NM_006636	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), nuclear gene encoding mitochondrial protein, mRNA
NM_022818	Homo sapiens microtubule-associated proteins 1A/1B light chain 3 (MAP1A/1BLC3), mRNA
NM_018607	Homo sapiens hypothetical protein PRO1853 (PRO1853), mRNA
NM_004856	Homo sapiens kinesin-like 5 (mitotic kinesin-like protein 1) (KNSL5), mRNA
NM_030979	Homo sapiens poly(A) binding protein, cytoplasmic 3 (PABPC3), mRNA
NM_030770	Homo sapiens transmembrane protease, serine 5 (spinesin) (TMPRSS5), mRNA
NM_002545	Homo sapiens opioid binding protein/cell adhesion molecule-like (OPCML), mRNA
NM_014676	Homo sapiens pumilio homolog 1 (Drosophila) (PUM1), mRNA
NM_030673	Homo sapiens SEC13-like 1 (S. cerevisiae) (SEC13L1), mRNA
NM_003342	Homo sapiens ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans) (UBE2G1), mRNA
NM_022051	Homo sapiens egl nine homolog 1 (C. elegans) (EGLN1), mRNA
NM_015577	Homo sapiens retinoic acid induced 14 (RAI14), mRNA
NM_012170	Homo sapiens F-box only protein 22 (FBXO22), mRNA
NM_022304	Homo sapiens histamine receptor H2 (HRH2), mRNA
NM_022333	Homo sapiens TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 2, mRNA
NM_003252	Homo sapiens TIA1 cytotoxic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 1, mRNA
NM_017910	Homo sapiens hypothetical protein FLJ20628 (FLJ20628), mRNA
NM_012384	Homo sapiens glucocorticoid modulatory element binding protein 2 (GMEB2), mRNA
NM_006118	Homo sapiens HS1 binding protein (HAX1), mRNA
NM_022740	Homo sapiens homeodomain interacting protein kinase 2 (HIPK2), mRNA
NM_002005	Homo sapiens feline sarcoma oncogene (FES), mRNA
NM_014757	Homo sapiens mastermind-like 1 (Drosophila) (MAML1), mRNA
NM_025136	Homo sapiens optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia) (OPA3), mRNA
NM_024505	Homo sapiens NADPH oxidase, EF hand calcium-binding domain 5 (NOX5), mRNA
NM_022362	Homo sapiens MMS19-like (MET18 homolog, S. cerevisiae) (MMS19L), mRNA
NM_000256	Homo sapiens myosin binding protein C, cardiac (MYBPC3), mRNA
NM_000276	Homo sapiens oculocerebrorenal syndrome of Lowe (OCRL), transcript variant a, mRNA
NM_001587	Homo sapiens oculocerebrorenal syndrome of Lowe (OCRL), transcript variant b, mRNA
NM_001407	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 3 (flamingo homolog, Drosophila) (CELSR3), mRNA

NM_001408	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) (CELSR2), mRNA
NM_005735	Homo sapiens ARP1 actin-related protein 1 homolog B, centractin beta (yeast) (ACTR1B), mRNA
NM_012254	Homo sapiens very long-chain acyl-CoA synthetase homolog 2 (VLCS-H2), mRNA
NM_012331	Homo sapiens methionine sulfoxide reductase A (MSRA), mRNA
NM_016596	Homo sapiens histone deacetylase 7A (HDAC7A), transcript variant 2, mRNA
NM_015401	Homo sapiens histone deacetylase 7A (HDAC7A), transcript variant 1, mRNA
NM_004082	Homo sapiens dynactin 1 (p150, glued homolog, Drosophila) (DCTN1), transcript variant 1, mRNA
NM_023019	Homo sapiens dynactin 1 (p150, glued homolog, Drosophila) (DCTN1), transcript variant 2, mRNA
NM_002893	Homo sapiens retinoblastoma binding protein 7 (RBBP7), mRNA
NM_023001	Homo sapiens retinoblastoma binding protein 1 (RBBP1), transcript variant 3, mRNA
NM_023000	Homo sapiens retinoblastoma binding protein 1 (RBBP1), transcript variant 2, mRNA
NM_002892	Homo sapiens retinoblastoma binding protein 1 (RBBP1), transcript variant 1, mRNA
NM_024408	Homo sapiens Notch homolog 2 (Drosophila) (NOTCH2), mRNA
NM_012311	Homo sapiens KIN, antigenic determinant of recA protein homolog (mouse) (KIN), mRNA
NM_021938	Homo sapiens bruno-like 5, RNA binding protein (Drosophila) (BRUNOL5), mRNA
NM_020180	Homo sapiens bruno-like 4, RNA binding protein (Drosophila) (BRUNOL4), mRNA
NM_005868	Homo sapiens BET1 homolog (S. cerevisiae) (BET1), mRNA
NM_002467	Homo sapiens v-myc myelocytomatosis viral oncogene homolog (avian) (MYC), mRNA
NM_022817	Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 1, mRNA
NM_003894	Homo sapiens period homolog 2 (Drosophila) (PER2), transcript variant 2, mRNA
NM_006660	Homo sapiens ClpX caseinolytic protease X homolog (E. coli) (CLPX), mRNA
NM_012394	Homo sapiens prefoldin 2 (PFDN2), mRNA
NM_004234	Homo sapiens zinc finger protein 93 homolog (mouse) (ZFP93), mRNA
NM_005870	Homo sapiens sin3-associated polypeptide, 18kD (SAP18), mRNA
NM_003350	Homo sapiens ubiquitin-conjugating enzyme E2 variant 2 (UBE2V2), mRNA
NM_022476	Homo sapiens fused toes homolog (mouse) (FTS), mRNA
NM_022444	Homo sapiens solute carrier family 13 (sodium/sulfate symporters), member 1 (SLC13A1), mRNA
NM_018127	Homo sapiens elaC homolog 2 (E. coli) (ELAC2), mRNA
NM_014317	Homo sapiens trans-prenyltransferase (TPT), mRNA
NM_022173	Homo sapiens TIA1 cytotoxic granule-associated RNA binding protein (TIA1), transcript variant 2, mRNA
NM_022037	Homo sapiens TIA1 cytotoxic granule-associated RNA binding protein (TIA1), transcript variant 1, mRNA
NM_004973	Homo sapiens jumonji homolog (mouse) (JMJ), mRNA
NM_021971	Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant 2, mRNA
NM_013334	Homo sapiens GDP-mannose pyrophosphorylase B (GMPPB), transcript variant

	1, mRNA
NM_013335	Homo sapiens GDP-mannose pyrophosphorylase A (GMPPA), mRNA
NM_021267	Homo sapiens LAG1 longevity assurance homolog 1 (S. cerevisiae) (LASS1), mRNA
NM_005811	Homo sapiens growth differentiation factor 11 (GDF11), mRNA
NM_005971	Homo sapiens FXYD domain-containing ion transport regulator 3 (FXYD3), transcript variant 1, mRNA
NM_021910	Homo sapiens FXYD domain-containing ion transport regulator 3 (FXYD3), transcript variant 2, mRNA
NM_022096	Homo sapiens ankyrin repeat domain 5 (ANKRD5), mRNA
NM_022073	Homo sapiens egl nine homolog 3 (C. elegans) (EGLN3), mRNA
NM_022047	Homo sapiens differentially expressed in FDCP 6 homolog (mouse) (DEF6), mRNA
NM_021778	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 2, mRNA
NM_021777	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 3, mRNA
NM_000152	Homo sapiens glucosidase, alpha; acid (Pompe disease, glycogen storage disease type II) (GAA), mRNA
NM_002910	Homo sapiens renin binding protein (RENBP), mRNA
NM_012072	Homo sapiens complement component 1, q subcomponent, receptor 1 (C1QR1), mRNA
NM_000534	Homo sapiens PMS1 postmeiotic segregation increased 1 (S. cerevisiae) (PMS1), mRNA
NM_005451	Homo sapiens enigma (LIM domain protein) (ENIGMA), mRNA
NM_021975	Homo sapiens v-rel reticuloendotheliosis viral oncogene homolog A, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3, p65 (avian) (RELA), mRNA
NM_021958	Homo sapiens H2.0-like homeo box 1 (Drosophila) (HLX1), mRNA
NM_004139	Homo sapiens lipopolysaccharide binding protein (LBP), mRNA
NM_005442	Homo sapiens eomesodermin homolog (Xenopus laevis) (EOMES), mRNA
NM_004187	Homo sapiens Smcx homolog, X chromosome (mouse) (SMCX), mRNA
NM_003170	Homo sapiens suppressor of Ty 6 homolog (S. cerevisiae) (SUPT6H), mRNA
NM_003062	Homo sapiens slit homolog 3 (Drosophila) (SLIT3), mRNA
NM_003068	Homo sapiens slug homolog, zinc finger protein (chicken) (SLUG), mRNA
NM_021824	Homo sapiens NIF3 NGG1 interacting factor 3-like 1 (S. pombe) (NIF3L1), mRNA
NM_021783	Homo sapiens ectodysplasin A2 isoform receptor (XEDAR), mRNA
NM_004196	Homo sapiens cyclin-dependent kinase-like 1 (CDC2-related kinase) (CDKL1), mRNA
NM_000535	Homo sapiens PMS2 postmeiotic segregation increased 2 (S. cerevisiae) (PMS2), mRNA
NM_002356	Homo sapiens myristoylated alanine-rich protein kinase C substrate (MARCKS), mRNA
NM_021728	Homo sapiens orthodenticle homolog 2 (Drosophila) (OTX2), mRNA
NM_014588	Homo sapiens visual system homeobox 1 homolog, CHX10-like (zebrafish) (VSX1), mRNA
NM_003503	Homo sapiens CDC7 cell division cycle 7-like 1 (S. cerevisiae) (CDC7L1), mRNA
NM_004059	Homo sapiens cysteine conjugate-beta lyase; cytoplasmic (glutamine transaminase K, kyneurenine aminotransferase) (CCBL1), mRNA
NM_020651	Homo sapiens pellino homolog 1 (Drosophila) (PELI1), mRNA

NM_018411	Homo sapiens hairless homolog (mouse) (HR), mRNA
NM_014569	Homo sapiens zinc finger protein 95 homolog (mouse) (ZFP95), mRNA
NM_012458	Homo sapiens translocase of inner mitochondrial membrane 13 homolog B (yeast) (TIMM13B), mRNA
NM_000672	Homo sapiens alcohol dehydrogenase 6 (class V) (ADH6), mRNA
NM_003603	Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 1, mRNA
NM_021069	Homo sapiens Arg/Abl-interacting protein ArgBP2 (ARGBP2), transcript variant 2, mRNA
NM_004950	Homo sapiens dermatan sulfate proteoglycan 3 (DSPG3), mRNA
NM_004701	Homo sapiens cyclin B2 (CCNB2), mRNA
NM_021100	Homo sapiens NFS1 nitrogen fixation 1 (S. cerevisiae) (NFS1), mRNA
NM_021255	Homo sapiens pellino homolog 2 (Drosophila) (PELI2), mRNA
NM_021115	Homo sapiens seizure related 6 homolog (mouse)-like (SEZ6L), mRNA
NM_004756	Homo sapiens numb homolog (Drosophila)-like (NUMBL), mRNA
NM_004690	Homo sapiens LATS, large tumor suppressor, homolog 1 (Drosophila) (LATS1), mRNA
NM_000461	Homo sapiens thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian) (THRB), mRNA
NM_021078	Homo sapiens GCN5 general control of amino-acid synthesis 5-like 2 (yeast) (GCN5L2), mRNA
NM_002877	Homo sapiens RAD51-like 1 (S. cerevisiae) (RAD51L1), mRNA
NM_001552	Homo sapiens insulin-like growth factor binding protein 4 (IGFBP4), mRNA
NM_002487	Homo sapiens necdin homolog (mouse) (NDN), mRNA
NM_012425	Homo sapiens Ras suppressor protein 1 (RSU1), mRNA
NM_005618	Homo sapiens delta-like 1 (Drosophila) (DLL1), mRNA
NM_021038	Homo sapiens muscleblind-like (Drosophila) (MBNL), mRNA
NM_014268	Homo sapiens microtubule-associated protein, RP/EB family, member 2 (MAPRE2), mRNA
NM_020662	Homo sapiens MRS2-like, magnesium homeostasis factor (S. cerevisiae) (MRS2L), mRNA
NM_020649	Homo sapiens chromobox homolog 8 (Pc class homolog, Drosophila) (CBX8), mRNA
NM_018436	Homo sapiens allantoicase (ALLC), mRNA
NM_020528	Homo sapiens poly(rC) binding protein 3 (PCBP3), mRNA
NM_014276	Homo sapiens recombining binding protein suppressor of hairless (Drosophila)-like (RBPSUHL), mRNA
NM_019557	Homo sapiens hypothetical protein RP1-317E23 (LOC56181), mRNA
NM_020347	Homo sapiens leucine zipper transcription factor-like 1 (LZTFL1), mRNA
NM_005744	Homo sapiens ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila) (ARIH1), mRNA
NM_007044	Homo sapiens katanin p60 (ATPase-containing) subunit A 1 (KATNA1), mRNA
NM_002688	Homo sapiens peanut-like 1 (Drosophila) (PNUTL1), mRNA
NM_013384	Homo sapiens LAG1 longevity assurance homolog 2 (S. cerevisiae) (LASS2), mRNA
NM_020230	Homo sapiens peter pan homolog (Drosophila) (PPAN), mRNA
NM_020182	Homo sapiens transmembrane, prostate androgen induced RNA (TMEPAI), mRNA
NM_020248	Homo sapiens catenin, beta interacting protein 1 (CTNNBIP1), mRNA
NM_000399	Homo sapiens early growth response 2 (Krox-20 homolog, Drosophila) (EGR2), mRNA
NM_002965	Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9),

	mRNA
NM_002964	Homo sapiens S100 calcium binding protein A8 (calgranulin A) (S100A8), mRNA
NM_002963	Homo sapiens S100 calcium binding protein A7 (psoriasin 1) (S100A7), mRNA
NM_014624	Homo sapiens S100 calcium binding protein A6 (calcyclin) (S100A6), mRNA
NM_019554	Homo sapiens S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), transcript variant 2, mRNA
NM_002961	Homo sapiens S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), transcript variant 1, mRNA
NM_005978	Homo sapiens S100 calcium binding protein A2 (S100A2), mRNA
NM_002537	Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2), mRNA
NM_019854	Homo sapiens HMT1 hnRNP methyltransferase-like 3 (S. cerevisiae) (HRMT1L3), mRNA
NM_019619	Homo sapiens par-3 partitioning defective 3 homolog (C. elegans) (PARD3), mRNA
NM_017454	Homo sapiens staufen, RNA binding protein (Drosophila) (STAU), transcript variant T1, mRNA
NM_017453	Homo sapiens staufen, RNA binding protein (Drosophila) (STAU), transcript variant T3, mRNA
NM_017452	Homo sapiens staufen, RNA binding protein (Drosophila) (STAU), transcript variant T2, mRNA
NM_003785	Homo sapiens G antigen, family B, 1 (prostate associated) (GAGEB1), mRNA
NM_015044	Homo sapiens golgi associated, gamma adaptin ear containing, ARF binding protein 2 (GGA2), mRNA
NM_013365	Homo sapiens golgi associated, gamma adaptin ear containing, ARF binding protein 1 (GGA1), mRNA
NM_004781	Homo sapiens vesicle-associated membrane protein 3 (cellubrevin) (VAMP3), mRNA
NM_018685	Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila) (ANLN), mRNA
NM_017927	Homo sapiens mitofusin 1 (MFN1), transcript variant 2, mRNA
NM_018387	Homo sapiens spermatid perinuclear RNA binding protein (STRBP), mRNA
NM_018378	Homo sapiens F-box and leucine-rich repeat protein 8 (FBXL8), mRNA
NM_018158	Homo sapiens solute carrier family 4 (anion exchanger), member 1, adaptor protein (SLC4A1AP), mRNA
NM_018032	Homo sapiens LUC7-like (S. cerevisiae) (LUC7L), mRNA
NM_017575	Homo sapiens chromosome 17 open reading frame 31 (C17orf31), mRNA
NM_018696	Homo sapiens elaC homolog 1 (E. coli) (ELAC1), mRNA
NM_005781	Homo sapiens activated p21cdc42Hs kinase (ACK1), mRNA
NM_016831	Homo sapiens period homolog 3 (Drosophila) (PER3), mRNA
NM_003387	Homo sapiens Wiskott-Aldrich syndrome protein interacting protein (WASPIP), mRNA
NM_005993	Homo sapiens tubulin-specific chaperone d (TBCD), mRNA
NM_003014	Homo sapiens secreted frizzled-related protein 4 (SFRP4), mRNA
NM_006744	Homo sapiens retinol binding protein 4, plasma (RBP4), mRNA
NM_002899	Homo sapiens retinol binding protein 1, cellular (RBP1), mRNA
NM_005524	Homo sapiens hairy homolog (Drosophila) (HRY), mRNA
NM_005206	Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian) (CRK), transcript variant I, mRNA
NM_016823	Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian) (CRK), transcript variant II, mRNA
NM_016948	Homo sapiens par-6 partitioning defective 6 homolog alpha (C.elegans)

	(PARD6A), mRNA
NM_017420	Homo sapiens sine oculis homeobox homolog 4 (Drosophila) (SIX4), mRNA
NM_016932	Homo sapiens sine oculis homeobox homolog 2 (Drosophila) (SIX2), mRNA
NM_017415	Homo sapiens kelch-like 3 (Drosophila) (KLHL3), mRNA
NM_017412	Homo sapiens frizzled homolog 3 (Drosophila) (FZD3), mRNA
NM_003400	Homo sapiens exportin 1 (CRM1 homolog, yeast) (XPO1), mRNA
NM_002889	Homo sapiens retinoic acid receptor responder (tazarotene induced) 2 (RARRES2), mRNA
NM_006064	Homo sapiens GTP-binding protein ragB (RAGB), transcript variant RAGBs, mRNA
NM_016656	Homo sapiens GTP-binding protein ragB (RAGB), transcript variant RAGBl, mRNA
NM_003857	Homo sapiens galanin receptor 2 (GALR2), mRNA
NM_016655	Homo sapiens GA binding protein transcription factor, beta subunit 2 (47kD) (GABPB2), transcript variant gamma, mRNA
NM_002041	Homo sapiens GA binding protein transcription factor, beta subunit 2 (47kD) (GABPB2), transcript variant gamma, mRNA
NM_016654	Homo sapiens GA binding protein transcription factor, beta subunit 1 (53kD) (GABPB1), transcript variant beta, mRNA
NM_005254	Homo sapiens GA binding protein transcription factor, beta subunit 1 (53kD) (GABPB1), transcript variant beta, mRNA
NM_015843	Homo sapiens LIM domain only 7 (LMO7), transcript variant 3, mRNA
NM_015842	Homo sapiens LIM domain only 7 (LMO7), transcript variant 2, mRNA
NM_002228	Homo sapiens v-jun sarcoma virus 17 oncogene homolog (avian) (JUN), mRNA
NM_016178	Homo sapiens ornithine decarboxylase antizyme 3 (OAZ3), mRNA
NM_016538	Homo sapiens sirtuin silent mating type information regulation 2 homolog 7 (S. cerevisiae) (SIRT7), mRNA
NM_016539	Homo sapiens sirtuin silent mating type information regulation 2 homolog 6 (S. cerevisiae) (SIRT6), mRNA
NM_016316	Homo sapiens REV1-like (yeast) (REV1L), mRNA
NM_016138	Homo sapiens COQ7 coenzyme Q, 7 homolog ubiquinone (yeast) (COQ7), mRNA
NM_016583	Homo sapiens palate, lung and nasal epithelium carcinoma associated (PLUNC), mRNA
NM_015886	Homo sapiens protease inhibitor 15 (PI15), mRNA
NM_016067	Homo sapiens mitochondrial ribosomal protein S18C (MRPS18C), nuclear gene encoding mitochondrial protein, mRNA
NM_015946	Homo sapiens pelota homolog (Drosophila) (PELO), mRNA
NM_016397	Homo sapiens TH1-like (Drosophila) (TH1L), mRNA
NM_016587	Homo sapiens chromobox homolog 3 (HP1 gamma homolog, Drosophila) (CBX3), mRNA
NM_016347	Homo sapiens putative N-acetyltransferase Camello 2 (CML2), mRNA
NM_015727	Homo sapiens tachykinin receptor 1 (TACR1), transcript variant short, mRNA
NM_001058	Homo sapiens tachykinin receptor 1 (TACR1), transcript variant long, mRNA
NM_004052	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 3 (BNIP3), nuclear gene encoding mitochondrial protein, mRNA
NM_014820	Homo sapiens translocase of outer mitochondrial membrane 70 homolog A (yeast) (TOMM70A), mRNA
NM_014918	Homo sapiens carbohydrate (chondroitin) synthase 1 (CHSY1), mRNA
NM_014707	Homo sapiens histone deacetylase 9 (HDAC9-PENDING), transcript variant 3, mRNA
NM_014683	Homo sapiens unc-51-like kinase 2 (C. elegans) (ULK2), mRNA

NM_014874	Homo sapiens mitofusin 2 (MFN2), mRNA
NM_014071	Homo sapiens nuclear receptor coactivator 6 (NCOA6), mRNA
NM_015700	Homo sapiens HIRA interacting protein 5 (HIRIP5), mRNA
NM_015685	Homo sapiens syndecan binding protein (syntenin) 2 (SDCBP2), mRNA
NM_014263	Homo sapiens YME1-like 1 (S. cerevisiae) (YME1L1), mRNA
NM_014297	Homo sapiens protein expressed in thyroid (YF13H12), mRNA
NM_014393	Homo sapiens staufen, RNA binding protein, homolog 2 (Drosophila) (STAU2), mRNA
NM_014403	Homo sapiens sialyltransferase 7D ((alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) (SIAT7D), mRNA
NM_014465	Homo sapiens sulfotransferase family, cytosolic, 1B, member 1 (SULT1B1), mRNA
NM_014485	Homo sapiens prostaglandin D2 synthase, hematopoietic (PGDS), mRNA
NM_014303	Homo sapiens pescadillo homolog 1, containing BRCT domain (zebrafish) (PES1), mRNA
NM_014253	Homo sapiens odz, odd Oz/ten-m homolog 1(Drosophila) (ODZ1), mRNA
NM_014429	Homo sapiens microrchidia homolog (mouse) (MORC), mRNA
NM_006439	Homo sapiens mab-21-like 2 (C. elegans) (MAB21L2), mRNA
NM_015322	Homo sapiens fem-1 homolog b (C. elegans) (FEM1B), mRNA
NM_014591	Homo sapiens Kv channel interacting protein 2 (KCNIP2), mRNA
NM_004449	Homo sapiens v-ets erythroblastosis virus E26 oncogene like (avian) (ERG), mRNA
NM_014420	Homo sapiens dickkopf homolog 4 (Xenopus laevis) (DKK4), mRNA
NM_014421	Homo sapiens dickkopf homolog 2 (Xenopus laevis) (DKK2), mRNA
NM_014325	Homo sapiens coronin, actin binding protein, 1C (CORO1C), mRNA
NM_014246	Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (CELSR1), mRNA
NM_014391	Homo sapiens cardiac ankyrin repeat protein (CARP), mRNA
NM_014336	Homo sapiens aryl hydrocarbon receptor interacting protein-like 1 (AIPL1), mRNA
NM_014265	Homo sapiens a disintegrin and metalloproteinase domain 28 (ADAM28), transcript variant 1, mRNA
NM_014237	Homo sapiens a disintegrin and metalloproteinase domain 18 (ADAM18), mRNA
NM_005032	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
NM_013980	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 1 (BNIP1), transcript variant BNIP1-c, mRNA
NM_013979	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 1 (BNIP1), transcript variant BNIP1-b, mRNA
NM_013978	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 1 (BNIP1), transcript variant BNIP1-a, mRNA
NM_004178	Homo sapiens TAR (HIV) RNA binding protein 2 (TARBP2), mRNA
NM_005915	Homo sapiens MCM6 minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisiae) (MCM6), mRNA
NM_002576	Homo sapiens p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast) (PAK1), mRNA
NM_012091	Homo sapiens adenosine deaminase, tRNA-specific 1 (ADAT1), mRNA
NM_005358	Homo sapiens LIM domain only 7 (LMO7), mRNA
NM_013451	Homo sapiens fer-1-like 3, myoferlin (C. elegans) (FER1L3), mRNA
NM_006113	Homo sapiens vav 3 oncogene (VAV3), mRNA
NM_003869	Homo sapiens carboxylesterase 2 (intestine, liver) (CES2), mRNA

NM_005721	Homo sapiens ARP3 actin-related protein 3 homolog (yeast) (ACTR3), mRNA
NM_003325	Homo sapiens HIR histone cell cycle regulation defective homolog A (S. cerevisiae) (HIRA), mRNA
NM_012242	Homo sapiens dickkopf homolog 1 (Xenopus laevis) (DKK1), mRNA
NM_012429	Homo sapiens SEC14-like 2 (S. cerevisiae) (SEC14L2), mRNA
NM_012190	Homo sapiens formyltetrahydrofolate dehydrogenase (FTHFD), mRNA
NM_005069	Homo sapiens single-minded homolog 2 (Drosophila) (SIM2), transcript variant SIM2, mRNA
NM_009586	Homo sapiens single-minded homolog 2 (Drosophila) (SIM2), transcript variant SIM2s, mRNA
NM_002610	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
NM_013374	Homo sapiens programmed cell death 6 interacting protein (PDCD6IP), mRNA
NM_013367	Homo sapiens anaphase-promoting complex subunit 4 (APC4), mRNA
NM_002968	Homo sapiens sal-like 1 (Drosophila) (SALL1), mRNA
NM_002449	Homo sapiens msh homeo box homolog 2 (Drosophila) (MSX2), mRNA
NM_006739	Homo sapiens MCM5 minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae) (MCM5), mRNA
NM_012460	Homo sapiens translocase of inner mitochondrial membrane 9 homolog (yeast) (TIMM9), mRNA
NM_012457	Homo sapiens translocase of inner mitochondrial membrane 13 homolog A (yeast) (TIMM13A), mRNA
NM_012456	Homo sapiens translocase of inner mitochondrial membrane 10 homolog (yeast) (TIMM10), mRNA
NM_012450	Homo sapiens solute carrier family 13 (sodium/sulfate symporters), member 4 (SLC13A4), mRNA
NM_012444	Homo sapiens SPO11 meiotic protein covalently bound to DSB-like (S. cerevisiae) (SPO11), mRNA
NM_012240	Homo sapiens sirtuin silent mating type information regulation 2 homolog 4 (S. cerevisiae) (SIRT4), mRNA
NM_012387	Homo sapiens peptidyl arginine deiminase, type V (PAD), mRNA
NM_012381	Homo sapiens origin recognition complex, subunit 3-like (yeast) (ORC3L), mRNA
NM_012225	Homo sapiens nucleotide binding protein 2 (MinD homolog, E. coli) (NUBP2), mRNA
NM_012222	Homo sapiens mutY homolog (E. coli) (MUTYH), mRNA
NM_012279	Homo sapiens double-stranded RNA-binding zinc finger protein JAZ (JAZ), mRNA
NM_012206	Homo sapiens hepatitis A virus cellular receptor 1 (HAVCR-1), mRNA
NM_012205	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
NM_012198	Homo sapiens grancalcin, EF-hand calcium binding protein (GCA), mRNA
NM_012193	Homo sapiens frizzled homolog 4 (Drosophila) (FZD4), mRNA
NM_012192	Homo sapiens fracture callus 1 homolog (rat) (FXC1), mRNA
NM_012076	Homo sapiens crumbs homolog 1 (Drosophila) (CRB1), mRNA
NM_012124	Homo sapiens cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1 (CHORDC1), mRNA
NM_012118	Homo sapiens CCR4 carbon catabolite repression 4-like (S. cerevisiae) (CCRN4L), mRNA
NM_012117	Homo sapiens chromobox homolog 5 (HP1 alpha homolog, Drosophila) (CBX5), mRNA
NM_012108	Homo sapiens BCR downstream signaling 1 (BRDG1), mRNA
NM_012100	Homo sapiens aspartyl aminopeptidase (DNPEP), mRNA

NM_012094	Homo sapiens peroxiredoxin 5 (PRDX5), mRNA
NM_004506	Homo sapiens heat shock transcription factor 2 (HSF2), mRNA
NM_004423	Homo sapiens dishevelled, dsh homolog 3 (Drosophila) (DVL3), mRNA
NM_007374	Homo sapiens sine oculis homeobox homolog 6 (Drosophila (SIX6), mRNA
NM_007373	Homo sapiens soc-2 suppressor of clear homolog (C. elegans) (SHOC2), mRNA
NM_002388	Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA
NM_004873	Homo sapiens BCL2-associated athanogene 5 (BAG5), mRNA
NM_007316	Homo sapiens agouti related protein homolog (mouse) (AGRP), transcript variant 2, mRNA
NM_003819	Homo sapiens poly(A) binding protein, cytoplasmic 4 (inducible form) (PABPC4), mRNA
NM_005737	Homo sapiens ADP-ribosylation factor-like 7 (ARL7), mRNA
NM_002358	Homo sapiens MAD2 mitotic arrest deficient-like 1 (yeast) (MAD2L1), mRNA
NM_007264	Homo sapiens adrenomedullin receptor (ADMR), mRNA
NM_006870	Homo sapiens destrin (actin depolymerizing factor) (DSTN), mRNA
NM_005476	Homo sapiens UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase (GNE), mRNA
NM_007309	Homo sapiens diaphanous homolog 2 (Drosophila) (DIAPH2), transcript variant 12C, mRNA
NM_001878	Homo sapiens cellular retinoic acid binding protein 2 (CRABP2), mRNA
NM_000489	Homo sapiens alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX), mRNA
NM_002528	Homo sapiens nth endonuclease III-like 1 (E. coli) (NTHL1), mRNA
NM_004085	Homo sapiens translocase of inner mitochondrial membrane 8 homolog A (yeast) (TIMM8A), nuclear gene encoding mitochondrial protein, mRNA
NM_002310	Homo sapiens leukemia inhibitory factor receptor (LIFR), mRNA
NM_004733	Homo sapiens acetyl-Coenzyme A transporter (ACATN), mRNA
NM_002657	Homo sapiens pleiomorphic adenoma gene-like 2 (PLAGL2), mRNA
NM_006724	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript variant 2, mRNA
NM_006882	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2e, mRNA
NM_006881	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2d, mRNA
NM_006880	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2c, mRNA
NM_006879	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2b, mRNA
NM_006878	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2a, mRNA
NM_003801	Homo sapiens GPAA1P anchor attachment protein 1 homolog (yeast) (GPAA1), mRNA
NM_003193	Homo sapiens tubulin-specific chaperone e (TBCE), mRNA
NM_002370	Homo sapiens mago-nashi homolog, proliferation-associated (Drosophila) (MAGOH), mRNA
NM_006341	Homo sapiens MAD2 mitotic arrest deficient-like 2 (yeast) (MAD2L2), mRNA
NM_006149	Homo sapiens lectin, galactoside-binding, soluble, 4 (galectin 4) (LGALS4), mRNA
NM_003585	Homo sapiens double C2-like domains, beta (DOC2B), mRNA
NM_007129	Homo sapiens Zic family member 2 (odd-paired homolog, Drosophila) (ZIC2), mRNA

NM_007279	Homo sapiens U2 small nuclear ribonucleoprotein auxiliary factor (65kD) (U2AF65), mRNA
NM_007194	Homo sapiens CHK2 checkpoint homolog (S. pombe) (CHEK2), mRNA
NM_007271	Homo sapiens serine/threonine kinase 38 (STK38), mRNA
NM_007232	Homo sapiens histamine receptor H3 (HRH3), mRNA
NM_007278	Homo sapiens GABA(A) receptor-associated protein (GABARAP), mRNA
NM_007197	Homo sapiens frizzled homolog 10 (Drosophila) (FZD10), mRNA
NM_007246	Homo sapiens kelch-like 2, Mayven (Drosophila) (KLHL2), mRNA
NM_001466	Homo sapiens frizzled homolog 2 (Drosophila) (FZD2), mRNA
NM_006482	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 2, mRNA
NM_003583	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2), transcript variant 1, mRNA
NM_006484	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B (DYRK1B), transcript variant c, mRNA
NM_006483	Homo sapiens dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B (DYRK1B), transcript variant b, mRNA
NM_001882	Homo sapiens corticotropin releasing hormone binding protein (CRHBP), mRNA
NM_005889	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 (APOBEC1), transcript variant 2, mRNA
NM_001644	Homo sapiens apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1 (APOBEC1), transcript variant 1, mRNA
NM_006936	Homo sapiens SMT3 suppressor of mif two 3 homolog 1 (yeast) (SMT3H1), mRNA
NM_006912	Homo sapiens Ric-like, expressed in many tissues (Drosophila) (RIT), mRNA
NM_006910	Homo sapiens retinoblastoma binding protein 6 (RBBP6), mRNA
NM_007068	Homo sapiens DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast) (DMC1), mRNA
NM_007021	Homo sapiens decidual protein induced by progesterone (DEPP), mRNA
NM_007007	Homo sapiens cleavage and polyadenylation specific factor 6, 68kD subunit (CPSF6), mRNA
NM_006822	Homo sapiens GTP-binding protein homologous to Saccharomyces cerevisiae SEC4 (SEC4L), mRNA
NM_006843	Homo sapiens serine dehydratase (SDS), mRNA
NM_006746	Homo sapiens sex comb on midleg-like 1 (Drosophila) (SCML1), mRNA
NM_006824	Homo sapiens EBNA1 binding protein 2 (EBNA1BP2), mRNA
NM_005922	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4), transcript variant 1, mRNA
NM_006807	Homo sapiens chromobox homolog 1 (HP1 beta homolog Drosophila) (CBX1), mRNA
NM_006734	Homo sapiens human immunodeficiency virus type I enhancer binding protein 2 (HIVEP2), mRNA
NM_006732	Homo sapiens FBJ murine osteosarcoma viral oncogene homolog B (FOSB), mRNA
NM_006729	Homo sapiens diaphanous homolog 2 (Drosophila) (DIAPH2), transcript variant 156, mRNA
NM_006829	Homo sapiens adipose specific 2 (APM2), mRNA
NM_006872	Homo sapiens TFIIA-alpha/beta-like factor (ALF), mRNA
NM_006796	Homo sapiens AFG3 ATPase family gene 3-like 2 (yeast) (AFG3L2), nuclear gene encoding mitochondrial protein, mRNA
NM_006544	Homo sapiens SEC10-like 1 (S. cerevisiae) (SEC10L1), mRNA

NM_006666	Homo sapiens RuvB-like 2 (E. coli) (RUVBL2), mRNA
NM_006509	Homo sapiens v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian) (RELB), mRNA
NM_006606	Homo sapiens retinoblastoma binding protein 9 (RBBP9), mRNA
NM_006620	Homo sapiens HBS1-like (S. cerevisiae) (HBS1L), mRNA
NM_006561	Homo sapiens CUG triplet repeat, RNA binding protein 2 (CUGBP2), mRNA
NM_006579	Homo sapiens emopamil binding protein (sterol isomerase) (EBP), mRNA
NM_006560	Homo sapiens CUG triplet repeat, RNA binding protein 1 (CUGBP1), mRNA
NM_001211	Homo sapiens BUB1 budding uninhibited by benzimidazoles 1 homolog beta (yeast) (BUB1B), mRNA
NM_006374	Homo sapiens serine/threonine kinase 25 (STE20 homolog, yeast) (STK25), mRNA
NM_006377	Homo sapiens unc-13-like (C. elegans) (UNC13), mRNA
NM_006357	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast) (UBE2E3), mRNA
NM_006323	Homo sapiens SEC24 related gene family, member B (S. cerevisiae) (SEC24B), mRNA
NM_006364	Homo sapiens Sec23 homolog A (S. cerevisiae) (SEC23A), mRNA
NM_006272	Homo sapiens S100 calcium binding protein, beta (neural) (S100B), mRNA
NM_006271	Homo sapiens S100 calcium binding protein A1 (S100A1), mRNA
NM_006391	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
NM_006265	Homo sapiens RAD21 homolog (S. pombe) (RAD21), mRNA
NM_006203	Homo sapiens phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D), mRNA
NM_006202	Homo sapiens phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila) (PDE4A), mRNA
NM_006190	Homo sapiens origin recognition complex, subunit 2-like (yeast) (ORC2L), mRNA
NM_006181	Homo sapiens netrin 2-like (chicken) (NTN2L), mRNA
NM_006168	Homo sapiens NK6 transcription factor homolog A (Drosophila) (NKX6A), mRNA
NM_006167	Homo sapiens NK3 transcription factor homolog A (Drosophila) (NKX3A), mRNA
NM_006159	Homo sapiens NEL-like 2 (chicken) (NELL2), mRNA
NM_006157	Homo sapiens NEL-like 1 (chicken) (NELL1), mRNA
NM_005360	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) (MAF), mRNA
NM_006306	Homo sapiens SMC1 structural maintenance of chromosomes 1-like 1 (yeast) (SMC1L1), mRNA
NM_006461	Homo sapiens mitotic spindle coiled-coil related protein (DEEPEST), mRNA
NM_006314	Homo sapiens connector enhancer of KSR-like (Drosophila kinase suppressor of ras) (CNK1), mRNA
NM_006366	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2), mRNA
NM_006444	Homo sapiens SMC2 structural maintenance of chromosomes 2-like 1 (yeast) (SMC2L1), mRNA
NM_006321	Homo sapiens ariadne homolog 2 (Drosophila) (ARIH2), mRNA
NM_006406	Homo sapiens peroxiredoxin 4 (PRDX4), mRNA
NM_006334	Homo sapiens olfactomedin 1 (OLFM1), transcript variant 2, mRNA
NM_004032	Homo sapiens D-aspartate oxidase (DDO), transcript variant 2, mRNA
NM_005985	Homo sapiens snail 1 homolog, zinc finger protein (Drosophila) (SNAI1), mRNA

NM_006109	Homo sapiens SKB1 homolog (S. pombe) (SKB1), mRNA
NM_005982	Homo sapiens sine oculis homeobox homolog 1 (Drosophila) (SIX1), mRNA
NM_006089	Homo sapiens sex comb on midleg-like 2 (Drosophila) (SCML2), mRNA
NM_005980	Homo sapiens S100 calcium binding protein P (S100P), mRNA
NM_005979	Homo sapiens S100 calcium binding protein A13 (S100A13), mRNA
NM_005938	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 7 (MLLT7), mRNA
NM_005937	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 (MLLT6), mRNA
NM_005936	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), mRNA
NM_005935	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 2 (MLLT2), mRNA
NM_005934	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 (MLLT1), mRNA
NM_005933	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) (MLL), mRNA
NM_005905	Homo sapiens MAD, mothers against decapentaplegic homolog 9 (Drosophila) (MADH9), mRNA
NM_005904	Homo sapiens MAD, mothers against decapentaplegic homolog 7 (Drosophila) (MADH7), mRNA
NM_005903	Homo sapiens MAD, mothers against decapentaplegic homolog 5 (Drosophila) (MADH5), mRNA
NM_005902	Homo sapiens MAD, mothers against decapentaplegic homolog 3 (Drosophila) (MADH3), mRNA
NM_005901	Homo sapiens MAD, mothers against decapentaplegic homolog 2 (Drosophila) (MADH2), mRNA
NM_005900	Homo sapiens MAD, mothers against decapentaplegic homolog 1 (Drosophila) (MADH1), mRNA
NM_006033	Homo sapiens lipase, endothelial (LIPG), mRNA
NM_006048	Homo sapiens ubiquitination factor E4B (UFD2 homolog, yeast) (UBE4B), mRNA
NM_006111	Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mitochondrial protein, mRNA
NM_006012	Homo sapiens ClpP caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli) (CLPP), nuclear gene encoding mitochondrial protein, mRNA
NM_006110	Homo sapiens CD2 antigen (cytoplasmic tail) binding protein 2 (CD2BP2), mRNA
NM_006017	Homo sapiens prominin-like 1 (mouse) (PROML1), mRNA
NM_004010	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427p2, mRNA
NM_004023	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp140bc, mRNA
NM_004022	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant D140ab, mRNA
NM_004021	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp140b, mRNA

NM_004020	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp140c, mRNA
NM_004019	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp40, mRNA
NM_004018	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp71ab, mRNA
NM_004017	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp71a, mRNA
NM_004016	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp71b, mRNA
NM_004015	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp71, mRNA
NM_004014	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp116, mRNA
NM_004013	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp140, mRNA
NM_004012	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp260-2, mRNA
NM_004011	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp260-1, mRNA
NM_004009	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427p1, mRNA
NM_004007	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427l, mRNA
NM_004006	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
NM_000109	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427c, mRNA
NM_005657	Homo sapiens tumor protein p53 binding protein, 1 (TP53BP1), mRNA
NM_005632	Homo sapiens small optic lobes homolog (Drosophila) (SOLH), mRNA
NM_005631	Homo sapiens smoothened homolog (Drosophila) (SMOH), mRNA
NM_005621	Homo sapiens S100 calcium binding protein A12 (calgranulin C) (S100A12), mRNA
NM_005620	Homo sapiens S100 calcium binding protein A11 (calgizzarin) (S100A11), mRNA
NM_005610	Homo sapiens retinoblastoma binding protein 4 (RBBP4), mRNA
NM_005732	Homo sapiens RAD50 homolog (S. cerevisiae) (RAD50), mRNA
NM_005591	Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), mRNA

NM_005590	Homo sapiens MRE11 meiotic recombination 11 homolog A (S. cerevisiae) (MRE11A), mRNA
NM_005585	Homo sapiens MAD, mothers against decapentaplegic homolog 6 (Drosophila) (MADH6), mRNA
NM_005584	Homo sapiens mab-21-like 1 (C. elegans) (MAB21L1), mRNA
NM_005582	Homo sapiens lymphocyte antigen 64 homolog, radioprotective 105kD (mouse) (LY64), mRNA
NM_005667	Homo sapiens zinc finger protein 103 homolog (mouse) (ZFP103), mRNA
NM_005886	Homo sapiens katanin p80 (WD40-containing) subunit B 1 (KATNB1), mRNA
NM_005860	Homo sapiens follistatin-like 3 (secreted glycoprotein) (FSTL3), mRNA
NM_005758	Homo sapiens heterogeneous nuclear ribonucleoprotein A3 (HNRPA3), mRNA
NM_005510	Homo sapiens dom-3 homolog Z (C. elegans) (DOM3Z), transcript variant 2, mRNA
NM_005766	Homo sapiens FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived) (FARP1), mRNA
NM_005722	Homo sapiens ARP2 actin-related protein 2 homolog (yeast) (ACTR2), mRNA
NM_005750	Homo sapiens chromosome 4 open reading frame 6 (C4orf6), mRNA
NM_005170	Homo sapiens achaete-scute complex-like 2 (Drosophila) (ASCL2), mRNA
NM_005426	Homo sapiens tumor protein p53 binding protein, 2 (TP53BP2), mRNA
NM_005486	Homo sapiens target of myb1-like 1 (chicken) (TOM1L1), mRNA
NM_005488	Homo sapiens target of myb1 (chicken) (TOM1), mRNA
NM_005417	Homo sapiens v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC), mRNA
NM_005413	Homo sapiens sine oculis homeobox homolog 3 (Drosophila) (SIX3), mRNA
NM_005444	Homo sapiens RCD1 required for cell differentiation1 homolog (S. pombe) (RQCD1), mRNA
NM_005378	Homo sapiens v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA
NM_005377	Homo sapiens v-myc myelocytomatosis viral oncogene homolog 2 (avian) (MYCL2), mRNA
NM_005375	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA
NM_005359	Homo sapiens MAD, mothers against decapentaplegic homolog 4 (Drosophila) (MADH4), mRNA
NM_005340	Homo sapiens histidine triad nucleotide binding protein (HINT), mRNA
NM_005307	Homo sapiens G protein-coupled receptor kinase 2-like (Drosophila) (GPRK2L), mRNA
NM_005262	Homo sapiens growth factor, augmenter of liver regeneration (ERV1 homolog, S. cerevisiae) (GFER), mRNA
NM_005261	Homo sapiens GTP binding protein overexpressed in skeletal muscle (GEM), mRNA
NM_005257	Homo sapiens GATA binding protein 6 (GATA6), mRNA
NM_005245	Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT), mRNA
NM_005244	Homo sapiens eyes absent homolog 2 (Drosophila) (EYA2), mRNA
NM_005239	Homo sapiens v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA
NM_005235	Homo sapiens v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) (ERBB4), mRNA
NM_005228	Homo sapiens epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian) (EGFR), mRNA
NM_005224	Homo sapiens dead ringer-like 1 (Drosophila) (DRIL1), mRNA
NM_005219	Homo sapiens diaphanous homolog 1 (Drosophila) (DIAPH1), mRNA

NM_005207	Homo sapiens v-crk sarcoma virus CT10 oncogene homolog (avian)-like (CRKL), mRNA
NM_005197	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
NM_005454	Homo sapiens cerberus 1 homolog, cysteine knot superfamily (Xenopus laevis) (CER1), mRNA
NM_005496	Homo sapiens SMC4 structural maintenance of chromosomes 4-like 1 (yeast) (SMC4L1), mRNA
NM_005169	Homo sapiens aristaless homeobox (Drosophila) (ARIX), mRNA
NM_005078	Homo sapiens transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila) (TLE3), mRNA
NM_005077	Homo sapiens transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila) (TLE1), mRNA
NM_005068	Homo sapiens single-minded homolog 1 (Drosophila) (SIM1), mRNA
NM_005067	Homo sapiens seven in absentia homolog 2 (Drosophila) (SIAH2), mRNA
NM_005138	Homo sapiens SCO cytochrome oxidase deficient homolog 2 (yeast) (SCO2), nuclear gene encoding mitochondrial protein, mRNA
NM_005156	Homo sapiens ROD1 regulator of differentiation 1 (S. pombe) (ROD1), mRNA
NM_005133	Homo sapiens RCE1 homolog, prenyl protein protease (S. cerevisiae) (RCE1), mRNA
NM_005057	Homo sapiens retinoblastoma binding protein 5 (RBBP5), mRNA
NM_005056	Homo sapiens retinoblastoma binding protein 2 (RBBP2), mRNA
NM_005053	Homo sapiens RAD23 homolog A (S. cerevisiae) (RAD23A), mRNA
NM_005049	Homo sapiens PWP2 periodic tryptophan protein homolog (yeast) (PWP2H), mRNA
NM_005008	Homo sapiens NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) (NHP2L1), mRNA
NM_004997	Homo sapiens myosin binding protein H (MYBPH), mRNA
NM_004677	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
NM_004788	Homo sapiens ubiquitination factor E4A (UFD2 homolog, yeast) (UBE4A), mRNA
NM_004617	Homo sapiens transmembrane 4 superfamily member 4 (TM4SF4), mRNA
NM_004607	Homo sapiens tubulin-specific chaperone a (TBCA), mRNA
NM_004602	Homo sapiens staufen, RNA binding protein (Drosophila) (STAU), transcript variant T4, mRNA
NM_004653	Homo sapiens Smcy homolog, Y chromosome (mouse) (SMCY), mRNA
NM_004787	Homo sapiens slit homolog 2 (Drosophila) (SLIT2), mRNA
NM_004593	Homo sapiens splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) (SFRS10), mRNA
NM_004206	Homo sapiens vesicle trafficking protein (SEC22C), transcript variant 2, mRNA
NM_004657	Homo sapiens serum deprivation response (phosphatidylserine binding protein) (SDPR), mRNA
NM_004589	Homo sapiens SCO cytochrome oxidase deficient homolog 1 (yeast) (SCO1), nuclear gene encoding mitochondrial protein, mRNA
NM_004587	Homo sapiens ribosome binding protein 1 homolog 180kD (dog) (RRBP1), mRNA
NM_004164	Homo sapiens retinol binding protein 2, cellular (RBP2), mRNA
NM_004584	Homo sapiens RAD9 homolog (S. pombe) (RAD9), mRNA
NM_004794	Homo sapiens RAB33A, member RAS oncogene family (RAB33A), mRNA
NM_004813	Homo sapiens peroxisomal biogenesis factor 16 (PEX16), transcript variant 1, mRNA
NM_004564	Homo sapiens PET112-like (yeast) (PET112L), mRNA
NM_004643	Homo sapiens poly(A) binding protein, nuclear 1 (PABPN1), mRNA

NM_004561	Homo sapiens ovo-like 1(Drosophila) (OVOL1), mRNA
NM_004153	Homo sapiens origin recognition complex, subunit 1-like (yeast) (ORC1L), mRNA
NM_004557	Homo sapiens Notch homolog 4 (Drosophila) (NOTCH4), mRNA
NM_004808	Homo sapiens N-myristoyltransferase 2 (NMT2), mRNA
NM_004210	Homo sapiens neuralized-like (Drosophila) (NEURL), mRNA
NM_004147	Homo sapiens developmentally regulated GTP binding protein 1 (DRG1), mRNA
NM_004851	Homo sapiens pronapsin A (NAP1), mRNA
NM_004533	Homo sapiens myosin binding protein C, fast type (MYBPC2), mRNA
NM_004529	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 (MLLT3), mRNA
NM_004668	Homo sapiens maltase-glucoamylase (alpha-glucosidase) (MGAM), mRNA
NM_004526	Homo sapiens MCM2 minichromosome maintenance deficient 2, mitotin (S. cerevisiae) (MCM2), mRNA
NM_004829	Homo sapiens lymphocyte antigen 94 homolog, activating NK-receptor; NK-p46, (mouse) (LY94), mRNA
NM_004744	Homo sapiens lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase) (LRAT), mRNA
NM_004524	Homo sapiens lethal giant larvae homolog 2 (Drosophila) (LLGL2), mRNA
NM_004140	Homo sapiens lethal giant larvae homolog 1 (Drosophila) (LLGL1), mRNA
NM_004922	Homo sapiens SEC24 related gene family, member C (S. cerevisiae) (SEC24C), mRNA
NM_004508	Homo sapiens isopentenyl-diphosphate delta isomerase (IDI1), mRNA
NM_004507	Homo sapiens HUS1 checkpoint homolog (S. pombe) (HUS1), mRNA
NM_004262	Homo sapiens airway trypsin-like protease (HAT), mRNA
NM_004752	Homo sapiens glial cells missing homolog b (Drosophila) (GCMB), mRNA
NM_004477	Homo sapiens FSHD region gene 1 (FRG1), mRNA
NM_004463	Homo sapiens faciogenital dysplasia (Aarskog-Scott syndrome) (FGD1), mRNA
NM_004106	Homo sapiens Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide (FCER1G), mRNA
NM_004456	Homo sapiens enhancer of zeste homolog 2 (Drosophila) (EZH2), mRNA
NM_004100	Homo sapiens eyes absent homolog 4 (Drosophila) (EYA4), mRNA
NM_004450	Homo sapiens enhancer of rudimentary homolog (Drosophila) (ERH), mRNA
NM_004448	Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (ERBB2), mRNA
NM_004445	Homo sapiens EphB6 (EPHB6), mRNA
NM_004436	Homo sapiens endosulfine alpha (ENSA), mRNA
NM_004432	Homo sapiens ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B) (ELAVL2), mRNA
NM_004230	Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 5 (EDG5), mRNA
NM_004421	Homo sapiens dishevelled, dsh homolog 1 (Drosophila) (DVL1), mRNA
NM_004399	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11), transcript variant 2, mRNA
NM_004378	Homo sapiens cellular retinoic acid binding protein 1 (CRABP1), mRNA
NM_004898	Homo sapiens clock homolog (mouse) (CLOCK), mRNA
NM_004669	Homo sapiens chloride intracellular channel 3 (CLIC3), mRNA
NM_004066	Homo sapiens centrin, EF-hand protein, 1 (CETN1), mRNA
NM_004354	Homo sapiens cyclin G2 (CCNG2), mRNA
NM_004352	Homo sapiens cerebellin 1 precursor (CBLN1), mRNA
NM_004057	Homo sapiens calbindin 3, (vitamin D-dependent calcium binding protein)

	(CALB3), mRNA
NM_004338	Homo sapiens chromosome 18 open reading frame 1 (C18orf1), mRNA
NM_004725	Homo sapiens BUB3 budding uninhibited by benzimidazoles 3 homolog (yeast) (BUB3), mRNA
NM_004336	Homo sapiens BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast) (BUB1), mRNA
NM_004331	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 3-like (BNIP3L), mRNA
NM_004328	Homo sapiens BCS1-like (yeast) (BCS1L), mRNA
NM_004045	Homo sapiens ATX1 antioxidant protein 1 homolog (yeast) (ATOX1), mRNA
NM_004849	Homo sapiens APG5 autophagy 5-like (S. cerevisiae) (APG5L), mRNA
NM_004674	Homo sapiens ash2 (absent, small, or homeotic)-like (Drosophila) (ASH2L), mRNA
NM_004316	Homo sapiens achaete-scute complex-like 1 (Drosophila) (ASCL1), mRNA
NM_004707	Homo sapiens APG12 autophagy 12-like (S. cerevisiae) (APG12L), mRNA
NM_004641	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 (MLLT10), mRNA
NM_004301	Homo sapiens BAF53 (BAF53A), mRNA
NM_001129	Homo sapiens AE binding protein 1 (AEBP1), mRNA
NM_003656	Homo sapiens calcium/calmodulin-dependent protein kinase I (CAMK1), mRNA
NM_000239	Homo sapiens lysozyme (renal amyloidosis) (LYZ), mRNA
NM_000456	Homo sapiens sulfite oxidase (SUOX), nuclear gene encoding mitochondrial protein, mRNA
NM_000435	Homo sapiens Notch homolog 3 (Drosophila) (NOTCH3), mRNA
NM_000251	Homo sapiens mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli) (MSH2), mRNA
NM_000249	Homo sapiens mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli) (MLH1), mRNA
NM_000210	Homo sapiens integrin, alpha 6 (ITGA6), mRNA
NM_001537	Homo sapiens heat shock factor binding protein 1 (HSBP1), mRNA
NM_001499	Homo sapiens GLE1 RNA export mediator-like (yeast) (GLE1L), mRNA
NM_001458	Homo sapiens filamin C, gamma (actin binding protein 280) (FLNC), mRNA
NM_001444	Homo sapiens fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA
NM_001432	Homo sapiens epiregulin (EREG), mRNA
NM_001388	Homo sapiens developmentally regulated GTP binding protein 2 (DRG2), mRNA
NM_001340	Homo sapiens cylicin, basic protein of sperm head cytoskeleton 2 (CYLC2), mRNA
NM_001326	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD (CSTF3), mRNA
NM_001325	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD (CSTF2), mRNA
NM_001324	Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD (CSTF1), mRNA
NM_001255	Homo sapiens CDC20 cell division cycle 20 homolog (S. cerevisiae) (CDC20), mRNA
NM_001122	Homo sapiens adipose differentiation-related protein (ADFP), mRNA
NM_003413	Homo sapiens Zic family member 3 heterotaxy 1 (odd-paired homolog, Drosophila) (ZIC3), mRNA
NM_003412	Homo sapiens Zic family member 1 (odd-paired homolog, Drosophila) (ZIC1), mRNA

NM_003408	Homo sapiens zinc finger protein 37 homolog (mouse) (ZFP37), mRNA
NM_003409	Homo sapiens zinc finger protein 161 homolog (mouse) (ZFP161), mRNA
NM_003680	Homo sapiens tyrosyl-tRNA synthetase (YARS), mRNA
NM_003390	Homo sapiens WEE1+ homolog (S. pombe) (WEE1), mRNA
NM_003565	Homo sapiens unc-51-like kinase 1 (C. elegans) (ULK1), mRNA
NM_003345	Homo sapiens ubiquitin-conjugating enzyme E2I (UBC9 homolog, yeast) (UBE2I), mRNA
NM_003344	Homo sapiens ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast) (UBE2H), mRNA
NM_003343	Homo sapiens ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast) (UBE2G2), mRNA
NM_003340	Homo sapiens ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) (UBE2D3), mRNA
NM_003338	Homo sapiens ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) (UBE2D1), mRNA
NM_003968	Homo sapiens ubiquitin-activating enzyme E1C (UBA3 homolog, yeast) (UBE1C), mRNA
NM_003320	Homo sapiens tubby homolog (mouse) (TUB), mRNA
NM_003278	Homo sapiens tetranectin (plasminogen binding protein) (TNA), mRNA
NM_003260	Homo sapiens transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila) (TLE2), mRNA
NM_003920	Homo sapiens timeless homolog (Drosophila) (TIMELESS), mRNA
NM_003251	Homo sapiens thyroid hormone responsive (SPOT14 homolog, rat) (THRSP), mRNA
NM_003250	Homo sapiens thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian) (THRA), mRNA
NM_003223	Homo sapiens transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4), mRNA
NM_003222	Homo sapiens transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) (TFAP2C), mRNA
NM_003221	Homo sapiens transcription factor AP-2 beta (activating enhancer binding protein 2 beta) (TFAP2B), mRNA
NM_003220	Homo sapiens transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha) (TFAP2A), mRNA
NM_000458	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), transcript variant a, mRNA
NM_003181	Homo sapiens T, brachyury homolog (mouse) (T), mRNA
NM_003173	Homo sapiens suppressor of variegation 3-9 homolog 1 (Drosophila) (SUV39H1), mRNA
NM_003171	Homo sapiens suppressor of var1, 3-like 1 (S. cerevisiae) (SUPV3L1), mRNA
NM_003169	Homo sapiens suppressor of Ty 5 homolog (S. cerevisiae) (SUPT5H), mRNA
NM_003168	Homo sapiens suppressor of Ty 4 homolog 1 (S. cerevisiae) (SUPT4H1), mRNA
NM_003599	Homo sapiens suppressor of Ty 3 homolog (S. cerevisiae) (SUPT3H), mRNA
NM_003162	Homo sapiens striatin, calmodulin binding protein (STRN), mRNA
NM_003134	Homo sapiens signal recognition particle 14kD (homologous Alu RNA binding protein) (SRP14), mRNA
NM_003088	Homo sapiens singed-like (fascin homolog, sea urchin) (Drosophila) (SNL), mRNA
NM_003061	Homo sapiens slit homolog 1 (Drosophila) (SLIT1), mRNA
NM_003036	Homo sapiens v-ski sarcoma viral oncogene homolog (avian) (SKI), mRNA
NM_003031	Homo sapiens seven in absentia homolog 1 (Drosophila) (SIAH1), mRNA
NM_000193	Homo sapiens sonic hedgehog homolog (Drosophila) (SHH), mRNA

NM_003003	Homo sapiens SEC14-like 1 (S. cerevisiae) (SEC14L1), mRNA
NM_002983	Homo sapiens small inducible cytokine A3 (SCYA3), mRNA
NM_002982	Homo sapiens small inducible cytokine A2 (monocyte chemotactic protein 1) (SCYA2), mRNA
NM_002981	Homo sapiens small inducible cytokine A1, I-309 (SCYA1), mRNA
NM_003864	Homo sapiens sin3-associated polypeptide, 30kD (SAP30), mRNA
NM_002962	Homo sapiens S100 calcium binding protein A5 (S100A5), mRNA
NM_002960	Homo sapiens S100 calcium binding protein A3 (S100A3), mRNA
NM_002966	Homo sapiens S100 calcium binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11)) (S100A10), mRNA
NM_003707	Homo sapiens RuvB-like 1 (E. coli) (RUVBL1), mRNA
NM_002944	Homo sapiens v-ros UR2 sarcoma virus oncogene homolog 1 (avian) (ROS1), mRNA
NM_002941	Homo sapiens roundabout, axon guidance receptor, homolog 1 (Drosophila) (ROBO1), mRNA
NM_000326	Homo sapiens retinaldehyde binding protein 1 (RLBP1), mRNA
NM_002930	Homo sapiens Ric-like, expressed in neurons (Drosophila) (RIN), mRNA
NM_003961	Homo sapiens rhomboid, veinlet-like 1 (Drosophila) (RHBDL), mRNA
NM_002912	Homo sapiens REV3-like, catalytic subunit of DNA polymerase zeta (yeast) (REV3L), mRNA
NM_002900	Homo sapiens retinol binding protein 3, interstitial (RBP3), mRNA
NM_002894	Homo sapiens retinoblastoma binding protein 8 (RBBP8), mRNA
NM_002888	Homo sapiens retinoic acid receptor responder (tazarotene induced) 1 (RARRES1), mRNA
NM_002879	Homo sapiens RAD52 homolog (S. cerevisiae) (RAD52), mRNA
NM_002878	Homo sapiens RAD51-like 3 (S. cerevisiae) (RAD51L3), mRNA
NM_002875	Homo sapiens RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae) (RAD51), mRNA
NM_002874	Homo sapiens RAD23 homolog B (S. cerevisiae) (RAD23B), mRNA
NM_002853	Homo sapiens RAD1 homolog (S. pombe) (RAD1), mRNA
NM_002873	Homo sapiens RAD17 homolog (S. pombe) (RAD17), mRNA
NM_000264	Homo sapiens patched homolog (Drosophila) (PTCH), mRNA
NM_003738	Homo sapiens patched homolog 2 (Drosophila) (PTCH2), mRNA
NM_002616	Homo sapiens period homolog 1 (Drosophila) (PER1), mRNA
NM_002600	Homo sapiens phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B), mRNA
NM_002568	Homo sapiens poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA
NM_003932	Homo sapiens suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) (ST13), mRNA
NM_003715	Homo sapiens vesicle docking protein p115 (P115), mRNA
NM_002553	Homo sapiens origin recognition complex, subunit 5-like (yeast) (ORC5L), mRNA
NM_002552	Homo sapiens origin recognition complex, subunit 4-like (yeast) (ORC4L), mRNA
NM_003634	Homo sapiens nipsnap homolog 1 (C. elegans) (NIPSNAP1), mRNA
NM_002499	Homo sapiens neogenin homolog 1 (chicken) (NEO1), mRNA
NM_002484	Homo sapiens nucleotide binding protein 1 (MinD homolog, E. coli) (NUBP1), mRNA
NM_003827	Homo sapiens N-ethylmaleimide-sensitive factor attachment protein, alpha (NAPA), mRNA
NM_002466	Homo sapiens v-myb myeloblastosis viral oncogene homolog (avian)-like 2 (MYBL2), mRNA

NM_002448	Homo sapiens msh homeo box homolog 1 (Drosophila) (MSX1), mRNA
NM_003576	Homo sapiens serine/threonine kinase 24 (STE20 homolog, yeast) (STK24), mRNA
NM_002442	Homo sapiens musashi homolog 1 (Drosophila) (MSI1), mRNA
NM_002441	Homo sapiens mutS homolog 5 (E. coli) (MSH5), mRNA
NM_002440	Homo sapiens mutS homolog 4 (E. coli) (MSH4), mRNA
NM_002439	Homo sapiens mutS homolog 3 (E. coli) (MSH3), mRNA
NM_002405	Homo sapiens manic fringe homolog (Drosophila) (MFNG), mRNA
NM_002402	Homo sapiens mesoderm specific transcript homolog (mouse) (MEST), mRNA
NM_002398	Homo sapiens Meis1, myeloid ecotropic viral integration site 1 homolog (mouse) (MEIS1), mRNA
NM_002393	Homo sapiens Mdm4, transformed 3T3 cell double minute 4, p53 binding protein (mouse) (MDM4), mRNA
NM_002392	Homo sapiens Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) (MDM2), transcript variant MDM2, mRNA
NM_003906	Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) associated protein (MCM3AP), mRNA
NM_002360	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian) (MAFK), mRNA
NM_002359	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian) (MAFG), mRNA
NM_003550	Homo sapiens MAD1 mitotic arrest deficient-like 1 (yeast) (MAD1L1), mRNA
NM_003937	Homo sapiens kynureninase (L-kynurenine hydrolase) (KYNU), mRNA
NM_002269	Homo sapiens karyopherin alpha 5 (importin alpha 6) (KPNA5), mRNA
NM_003772	Homo sapiens jerky homolog-like (mouse) (JRKL), mRNA
NM_002202	Homo sapiens ISL1 transcription factor, LIM/homeodomain, (islet-1) (ISL1), mRNA
NM_003604	Homo sapiens insulin receptor substrate 4 (IRS4), mRNA
NM_001570	Homo sapiens interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA
NM_003866	Homo sapiens inositol polyphosphate-4-phosphatase, type II, 105kD (INPP4B), mRNA
NM_001536	Homo sapiens HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae) (HRMT1L2), mRNA
NM_001535	Homo sapiens HMT1 hnRNP methyltransferase-like 1 (S. cerevisiae) (HRMT1L1), mRNA
NM_003806	Homo sapiens harakiri, BCL2 interacting protein (contains only BH3 domain) (HRK), mRNA
NM_002152	Homo sapiens histidine rich calcium binding protein (HRC), mRNA
NM_002114	Homo sapiens human immunodeficiency virus type I enhancer binding protein 1 (HIVEP1), mRNA
NM_003710	Homo sapiens serine protease inhibitor, Kunitz type 1 (SPINT1), mRNA
NM_000179	Homo sapiens mutS homolog 6 (E. coli) (MSH6), mRNA
NM_000839	Homo sapiens glutamate receptor, metabotropic 2 (GRM2), mRNA
NM_002077	Homo sapiens golgi autoantigen, golgin subfamily a, 1 (GOLGA1), mRNA
NM_003878	Homo sapiens gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase) (GGH), mRNA
NM_001488	Homo sapiens transcriptional adaptor 2 (ADA2 homolog, yeast)-like (TADA2L), mRNA
NM_001487	Homo sapiens GCN5 general control of amino-acid synthesis 5-like 1 (yeast) (GCN5L1), mRNA
NM_003643	Homo sapiens glial cells missing homolog a (Drosophila) (GCMA), mRNA
NM_002052	Homo sapiens GATA binding protein 4 (GATA4), mRNA

NM_002051	Homo sapiens GATA binding protein 3 (GATA3), mRNA
NM_002050	Homo sapiens GATA binding protein 2 (GATA2), mRNA
NM_002049	Homo sapiens GATA binding protein 1 (globin transcription factor 1) (GATA1), mRNA
NM_002040	Homo sapiens GA binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
NM_002039	Homo sapiens GRB2-associated binding protein 1 (GAB1), mRNA
NM_003508	Homo sapiens frizzled homolog 9 (Drosophila) (FZD9), mRNA
NM_003507	Homo sapiens frizzled homolog 7 (Drosophila) (FZD7), mRNA
NM_003506	Homo sapiens frizzled homolog 6 (Drosophila) (FZD6), mRNA
NM_003468	Homo sapiens frizzled homolog 5 (Drosophila) (FZD5), mRNA
NM_003505	Homo sapiens frizzled homolog 1 (Drosophila) (FZD1), mRNA
NM_001465	Homo sapiens FYN binding protein (FYB-120/130) (FYB), mRNA
NM_002031	Homo sapiens fyn-related kinase (FRK), mRNA
NM_003717	Homo sapiens neuropeptide FF-amide peptide precursor (NPFF), mRNA
NM_001457	Homo sapiens filamin B, beta (actin binding protein 278) (FLNB), mRNA
NM_001456	Homo sapiens filamin A, alpha (actin binding protein 280) (FLNA), mRNA
NM_002018	Homo sapiens flightless I homolog (Drosophila) (FLII), mRNA
NM_001991	Homo sapiens enhancer of zeste homolog 1 (Drosophila) (EZH1), mRNA
NM_001990	Homo sapiens eyes absent homolog 3 (Drosophila) (EYA3), mRNA
NM_000503	Homo sapiens eyes absent homolog 1 (Drosophila) (EYA1), mRNA
NM_001989	Homo sapiens eve, even-skipped homeo box homolog 1 (Drosophila) (EVX1), mRNA
NM_001982	Homo sapiens v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) (ERBB3), mRNA
NM_003584	Homo sapiens dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (DUSP11), mRNA
NM_003859	Homo sapiens dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (DPM1), mRNA
NM_001928	Homo sapiens D component of complement (adipsin) (DF), mRNA
NM_003649	Homo sapiens D-aspartate oxidase (DDO), transcript variant 1, mRNA
NM_001343	Homo sapiens disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) (DAB2), mRNA
NM_001913	Homo sapiens cut-like 1, CCAAT displacement protein (Drosophila) (CUTL1), mRNA
NM_001316	Homo sapiens CSE1 chromosome segregation 1-like (yeast) (CSE1L), mRNA
NM_003652	Homo sapiens carboxypeptidase Z (CPZ), mRNA
NM_003909	Homo sapiens copine III (CPNE3), mRNA
NM_003915	Homo sapiens copine I (CPNE1), mRNA
NM_001308	Homo sapiens carboxypeptidase N, polypeptide 1, 50kD (CPN1), mRNA
NM_001841	Homo sapiens cannabinoid receptor 2 (macrophage) (CNR2), mRNA
NM_001280	Homo sapiens cold inducible RNA binding protein (CIRBP), mRNA
NM_001274	Homo sapiens CHK1 checkpoint homolog (S. pombe) (CHEK1), mRNA
NM_001806	Homo sapiens CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG), mRNA
NM_003655	Homo sapiens chromobox homolog 4 (Pc class homolog, Drosophila) (CBX4), mRNA
NM_001749	Homo sapiens calpain, small subunit 1 (CAPNS1), mRNA
NM_000716	Homo sapiens complement component 4 binding protein, beta (C4BPB), mRNA
NM_000715	Homo sapiens complement component 4 binding protein, alpha (C4BPA), mRNA
NM_001726	Homo sapiens bromodomain, testis-specific (BRDT), mRNA

NM_001205	Homo sapiens BCL2/adenovirus E1B 19kD interacting protein 1 (BNIP1), transcript variant BNIP1, mRNA
NM_001714	Homo sapiens Bicaudal D homolog 1 (Drosophila) (BICD1), mRNA
NM_003766	Homo sapiens beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) (BECN1), mRNA
NM_003567	Homo sapiens breast cancer anti-estrogen resistance 3 (BCAR3), mRNA
NM_001189	Homo sapiens bagpipe homeobox homolog 1 (Drosophila) (BAPX1), mRNA
NM_001698	Homo sapiens AU RNA binding protein/enoyl-Coenzyme A hydratase (AUH), nuclear gene encoding mitochondrial protein, mRNA
NM_001672	Homo sapiens agouti signaling protein, nonagouti homolog (mouse) (ASIP), mRNA
NM_001638	Homo sapiens apolipoprotein F (APOF), mRNA
NM_003977	Homo sapiens aryl hydrocarbon receptor interacting protein (AIP), mRNA
NM_001138	Homo sapiens agouti related protein homolog (mouse) (AGRP), transcript variant 1, mRNA
NM_058246	Homo sapiens DnaJ (Hsp40) homolog, subfamily B, member 6 (DNAJB6), mRNA
NM_025225	Homo sapiens hypothetical protein dJ796I17.1 (DJ796I17.1), mRNA
NM_058165	Homo sapiens diacylglycerol acyltransferase 2-like (DGAT2-like), mRNA
NM_001861	Homo sapiens cytochrome c oxidase subunit IV isoform 1 (COX4I1), nuclear gene encoding mitochondrial protein, mRNA
NM_014491	Homo sapiens forkhead box P2 (FOXP2), mRNA
NM_054110	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7), mRNA
NM_006726	Homo sapiens vesicle trafficking, beach and anchor containing (LRBA), mRNA
NM_020663	Homo sapiens TC10-like Rho GTPase (TCL), mRNA
NM_020919	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) (ALS2), mRNA
NM_052852	Homo sapiens hypothetical zinc finger protein MGC2396 (MGC2396), mRNA
NM_053043	Homo sapiens hypothetical protein MGC20460 (MGC20460), mRNA
NM_053017	Homo sapiens ADP-ribosyltransferase 5 (ART5), mRNA
NM_052999	Homo sapiens chemokine-like factor-like protein CKLFH1 (CKLFH1), mRNA
NM_052881	Homo sapiens hypothetical protein dJ734P14.5 (novel C2H2 type zinc finger protein) (MGC20504), mRNA
NM_052968	Homo sapiens apolipoprotein A-V (APOA5), mRNA
NM_052960	Homo sapiens retinoid binding protein 7 (RBP7), mRNA
NM_052959	Homo sapiens pannexin 3 (PANX3), mRNA
NM_052948	Homo sapiens sorting nexin 26 (SNX26), mRNA
NM_052947	Homo sapiens heart alpha-kinase (HAK), mRNA
NM_052946	Homo sapiens hypothetical protein MGC20702 (MGC20702), mRNA
NM_052943	Homo sapiens hypothetical protein MGC16491 (MGC16491), mRNA
NM_052941	Homo sapiens guanylate binding protein 4 (GBP4), mRNA
NM_052935	Homo sapiens hypothetical protein MGC20781 (MGC20781), mRNA
NM_052890	Homo sapiens peptidoglycan recognition protein L precursor (PGLYRP), mRNA
NM_052885	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 13 (SLC2A13), mRNA
NM_052884	Homo sapiens sialic acid binding Ig-like lectin 11 (SIGLEC11), mRNA
NM_052877	Homo sapiens similar to hypothetical protein MNCb-2386 (MGC17544), mRNA
NM_052876	Homo sapiens transcriptional repressor NAC1 (NAC1), mRNA
NM_052873	Homo sapiens MGC16028 similar to RIKEN cDNA 1700019E19 gene (MGC16028), mRNA
NM_052871	Homo sapiens hypothetical protein MGC4677 (MGC4677), mRNA
NM_052870	Homo sapiens sorting nexin 18 (SNX18), mRNA

NM_052859	Homo sapiens putative endoplasmic reticulum multispan transmembrane protein (RFT1), mRNA
NM_052858	Homo sapiens similar to RIKEN cDNA 1810006A16 gene (LOC91862), mRNA
NM_052855	Homo sapiens hypothetical protein MGC15396 (MGC15396), mRNA
NM_052854	Homo sapiens old astrocyte specifically induced substance (OASIS), mRNA
NM_052844	Homo sapiens hypothetical protein MGC20486 (MGC20486), mRNA
NM_052839	Homo sapiens pannexin 2 (PANX2), mRNA
NM_033551	Homo sapiens hypothetical protein MGC19556 (MGC19556), mRNA
NM_033549	Homo sapiens hypothetical gene MGC1127 (MGC1127), mRNA
NM_033546	Homo sapiens myosin regulatory light chain (MLC-B), mRNA
NM_033544	Homo sapiens similar to cyclin-E binding protein 1 (H. sapiens) (MGC14386), mRNA
NM_033515	Homo sapiens MacGAP protein (MacGAP), mRNA
NM_033519	Homo sapiens olfactory receptor sdolf (sdolf), mRNA
NM_033516	Homo sapiens protein kinase NYD-SP25 (NYD-SP25), mRNA
NM_032231	Homo sapiens hypothetical protein FLJ22875 (FLJ22875), mRNA
NM_018437	Homo sapiens hypothetical protein EDAG-1 (EDAG-1), mRNA
NM_033378	Homo sapiens chorionic gonadotropin, beta polypeptide 2 (CGB2), mRNA
NM_033377	Homo sapiens chorionic gonadotropin, beta polypeptide 1 (CGB1), mRNA
NM_033448	Homo sapiens keratin 6 irs (KRT6IRS), mRNA
NM_033424	Homo sapiens similar to MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM (MYHC-ALPHA) (M. musculus) (LOC92771), mRNA
NM_033445	Homo sapiens similar to H2A histone family, member A (H. sapiens) (MGC3165), mRNA
NM_033439	Homo sapiens DVS27-related protein (DVS27), mRNA
NM_033440	Homo sapiens elastase 2A (ELA2A), mRNA
NM_033438	Homo sapiens CD84-H1 precursor (CD84-H1), mRNA
NM_033423	Homo sapiens similar to granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (H. sapiens) (CTLA1), mRNA
NM_033411	Homo sapiens hypothetical protein MGC13523 (MGC13523), mRNA
NM_033416	Homo sapiens similar to HYPOTHETICAL 34.0 KDA PROTEIN ZK795.3 IN CHROMOSOME IV (MGC19606), mRNA
NM_033413	Homo sapiens hypothetical gene MGC16309 (MGC16309), mRNA
NM_033410	Homo sapiens hypothetical protein MGC13138 (MGC13138), mRNA
NM_033419	Homo sapiens hypothetical gene MGC9753 (MGC9753), mRNA
NM_014083	Homo sapiens PRO0767 protein (PRO0767), mRNA
NM_033043	Homo sapiens chorionic gonadotropin, beta polypeptide 5 (CGB5), mRNA
NM_031451	Homo sapiens hypothetical protein MGC4766 similar to testis specific protein TES101RP (MGC4766), mRNA
NM_033183	Homo sapiens chorionic gonadotropin, beta polypeptide 8 (CGB8), mRNA
NM_020443	Homo sapiens hypothetical protein MGC14961 (MGC14961), mRNA
NM_033343	Homo sapiens LIM homeobox protein 4 (LHX4), mRNA
NM_033318	Homo sapiens hypothetical gene supported by AL449243 (LOC91689), mRNA
NM_033328	Homo sapiens capping protein alpha 3 (CAPPA3), mRNA
NM_033315	Homo sapiens ras-like protein VTS58635 (VTS58635), mRNA
NM_033309	Homo sapiens hypothetical protein MGC4655 (MGC4655), mRNA
NM_033296	Homo sapiens T-cell activation protein (PGR1), mRNA
NM_033297	Homo sapiens leucine-rich-repeat protein (RNO2), mRNA
NM_033280	Homo sapiens similar to signal peptidase complex (18kD) (LOC90701), mRNA
NM_033196	Homo sapiens similar to ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1) (H. sapiens) (LOC91120), mRNA
NM_033272	Homo sapiens potassium channel subunit HERG-3 (HERG-3), mRNA

NM_033261	Homo sapiens diphosphate dimethylallyl diphosphate isomerase 2 (IDI2), mRNA
NM_033254	Homo sapiens brother of CDO (BOC), mRNA
NM_033204	Homo sapiens hypothetical gene DKFZp570I0164 (DKFZp570I0164), mRNA
NM_033259	Homo sapiens CaM-KII inhibitory protein (CAM-KIIN), mRNA
NM_032597	Homo sapiens testes development-related NYD-SP21 (NYD-SP21), mRNA
NM_033212	Homo sapiens hypothetical gene supported by BC004307; BC008285 (MGC10992), mRNA
NM_033208	Homo sapiens similar to jerky (mouse) homolog-like (LOC91151), mRNA
NM_033195	Homo sapiens lactate dehydrogenase A -like (LDHL), mRNA
NM_015643	Homo sapiens DKFZP434F122 protein (DKFZP434F122), mRNA
NM_032604	Homo sapiens lung alpha/beta hydrolase 1 (LABH1), mRNA
NM_032133	Homo sapiens hypothetical protein DKFZp434N1415 (DKFZP434N1415), mRNA
NM_030803	Homo sapiens hypothetical protein FLJ10035 (FLJ10035), mRNA
NM_024062	Homo sapiens hypothetical protein MGC5338 (MGC5338), mRNA
NM_024059	Homo sapiens hypothetical protein MGC5356 (MGC5356), mRNA
NM_016542	Homo sapiens serine/threonine protein kinase MASK (MST4), mRNA
NM_033127	Homo sapiens regucalcin gene promotor region related protein (RGPR), mRNA
NM_033128	Homo sapiens scinderin (SCIN), mRNA
NM_033058	Homo sapiens ring finger protein 29 (RNF29), mRNA
NM_033116	Homo sapiens hypothetical protein MGC16714 (MGC16714), mRNA
NM_033123	Homo sapiens testis-development related NYD-SP27 (NYD-SP27), mRNA
NM_033126	Homo sapiens serine/threonine kinase PSKH2 (PSKH2), mRNA
NM_033124	Homo sapiens NYD-SP28 protein (NYD-SP28), mRNA
NM_033122	Homo sapiens testis development protein NYD-SP26 (NYD-SP26), mRNA
NM_033114	Homo sapiens MADP-1 protein (MADP-1), mRNA
NM_033083	Homo sapiens EAF1 protein (EAF1), mRNA
NM_033087	Homo sapiens hypothetical protein FLJ14511 (FLJ14511), mRNA
NM_024512	Homo sapiens leucine-rich repeat-containing 2 (LRRC2), mRNA
NM_006029	Homo sapiens paraneoplastic antigen MA1 (PNMA1), mRNA
NM_033025	Homo sapiens hypothetical protein FLJ13511 (7h3), mRNA
NM_015169	Homo sapiens homolog of yeast ribosome biogenesis regulatory protein RRS1 (RRS1), mRNA
NM_015129	Homo sapiens septin 6 (SEP2), mRNA
NM_032838	Homo sapiens hypothetical protein FLJ14779 (FLJ14779), mRNA
NM_032206	Homo sapiens hypothetical protein FLJ21709 (FLJ21709), mRNA
NM_032797	Homo sapiens hypothetical protein FLJ14497 (FLJ14497), mRNA
NM_032472	Homo sapiens peptidylprolyl isomerase (cyclophilin)-like 3 (PPIL3), mRNA
NM_032936	Homo sapiens DC32 (DC32), mRNA
NM_032577	Homo sapiens melanoma-associated chondroitin sulfate proteoglycan-like (LOC84664), mRNA
NM_032933	Homo sapiens hypothetical protein MGC11386 (MGC11386), mRNA
NM_032929	Homo sapiens hypothetical protein MGC14793 (MGC14793), mRNA
NM_032928	Homo sapiens hypothetical protein MGC14141 (MGC14141), mRNA
NM_032927	Homo sapiens hypothetical protein MGC13159 (MGC13159), mRNA
NM_032926	Homo sapiens hypothetical protein MGC15737 (MGC15737), mRNA
NM_032921	Homo sapiens hypothetical protein MGC15875 (MGC15875), mRNA
NM_032909	Homo sapiens hypothetical protein MGC14139 (MGC14139), mRNA
NM_032908	Homo sapiens hypothetical protein MGC14407 (MGC14407), mRNA
NM_032906	Homo sapiens hypothetical protein MGC14156 (MGC14156), mRNA
NM_032905	Homo sapiens hypothetical protein MGC14439 (MGC14439), mRNA
NM_032903	Homo sapiens hypothetical protein MGC14425 (MGC14425), mRNA

NM_032902	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 16A (PPP1R16A), mRNA
NM_032901	Homo sapiens hypothetical protein MGC14288 (MGC14288), mRNA
NM_032899	Homo sapiens hypothetical protein MGC14128 (MGC14128), mRNA
NM_032898	Homo sapiens hypothetical protein MGC14126 (MGC14126), mRNA
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NM_032892	Homo sapiens hypothetical protein MGC14161 (MGC14161), mRNA
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NM_032887	Homo sapiens hypothetical protein MGC16037 (MGC16037), mRNA
NM_032885	Homo sapiens hypothetical protein MGC15906 (MGC15906), mRNA
NM_032882	Homo sapiens hypothetical protein MGC15827 (MGC15827), mRNA
NM_032881	Homo sapiens U7 snRNP-specific Sm-like protein LSM10 (LSM10), mRNA
NM_032880	Homo sapiens hypothetical protein MGC15730 (MGC15730), mRNA
NM_032878	Homo sapiens hypothetical protein MGC15677 (MGC15677), mRNA
NM_032873	Homo sapiens hypothetical protein MGC15437 (MGC15437), mRNA
NM_032867	Homo sapiens hypothetical protein FLJ14966 (FLJ14966), mRNA
NM_032865	Homo sapiens hypothetical protein FLJ14950 (FLJ14950), mRNA
NM_032861	Homo sapiens hypothetical protein FLJ14917 (FLJ14917), mRNA
NM_032859	Homo sapiens hypothetical protein FLJ14906 (FLJ14906), mRNA
NM_032856	Homo sapiens hypothetical protein FLJ14888 (FLJ14888), mRNA
NM_032855	Homo sapiens hematopoietic SH2 protein (HSH2), mRNA
NM_032854	Homo sapiens hypothetical protein FLJ14871 (FLJ14871), mRNA
NM_032850	Homo sapiens hypothetical protein FLJ14840 (FLJ14840), mRNA
NM_032849	Homo sapiens hypothetical protein FLJ14834 (FLJ14834), mRNA
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NM_032843	Homo sapiens hypothetical protein FLJ14810 (FLJ14810), mRNA
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NM_032837	Homo sapiens hypothetical protein FLJ14775 (FLJ14775), mRNA
NM_032836	Homo sapiens hypothetical protein FLJ14768 (FLJ14768), mRNA
NM_032834	Homo sapiens hypothetical protein FLJ14751 (FLJ14751), mRNA
NM_032833	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 15B (PPP1R15B), mRNA
NM_032832	Homo sapiens hypothetical protein FLJ14735 (FLJ14735), mRNA
NM_032831	Homo sapiens CAP-binding protein complex interacting protein 2 (CBCIP2), mRNA
NM_032830	Homo sapiens hypothetical protein FLJ14728 (FLJ14728), mRNA
NM_032829	Homo sapiens hypothetical protein FLJ14721 (FLJ14721), mRNA
NM_032828	Homo sapiens ubiquitin UBF-fl (UBF-fl), mRNA
NM_032827	Homo sapiens hypothetical protein FLJ14708 (FLJ14708), mRNA
NM_032826	Homo sapiens hypothetical protein FLJ14697 (FLJ14697), mRNA
NM_032825	Homo sapiens hypothetical protein FLJ14686 (FLJ14686), mRNA
NM_032821	Homo sapiens hypothetical protein FLJ14665 (FLJ14665), mRNA
NM_032817	Homo sapiens hypothetical protein FLJ14641 (FLJ14641), mRNA
NM_032816	Homo sapiens hypothetical protein FLJ14640 (FLJ14640), mRNA
NM_032814	Homo sapiens hypothetical protein FLJ14627 (FLJ14627), mRNA
NM_032811	Homo sapiens hypothetical protein FLJ14621 (FLJ14621), mRNA

NM_032810	Homo sapiens hypothetical protein FLJ14600 (FLJ14600), mRNA
NM_032809	Homo sapiens hypothetical protein FLJ14596 (FLJ14596), mRNA
NM_032808	Homo sapiens hypothetical protein FLJ14594 (FLJ14594), mRNA
NM_032807	Homo sapiens hypothetical protein FLJ14590 (FLJ14590), mRNA
NM_032806	Homo sapiens hypothetical protein FLJ14566 (FLJ14566), mRNA
NM_032805	Homo sapiens hypothetical protein FLJ14549 (FLJ14549), mRNA
NM_032802	Homo sapiens hypothetical protein FLJ14540 (FLJ14540), mRNA
NM_032799	Homo sapiens hypothetical protein FLJ14524 (FLJ14524), mRNA
NM_032796	Homo sapiens reserved (SYAP1), mRNA
NM_032792	Homo sapiens hypothetical protein FLJ14486 (FLJ14486), mRNA
NM_032790	Homo sapiens hypothetical protein FLJ14466 (FLJ14466), mRNA
NM_032788	Homo sapiens hypothetical protein FLJ14457 (FLJ14457), mRNA
NM_032787	Homo sapiens hypothetical protein FLJ14454 (FLJ14454), mRNA
NM_032786	Homo sapiens hypothetical protein FLJ14451 (FLJ14451), mRNA
NM_032785	Homo sapiens hypothetical protein FLJ14442 (FLJ14442), mRNA
NM_032781	Homo sapiens hypothetical protein FLJ14427 (FLJ14427), mRNA
NM_032780	Homo sapiens hypothetical protein FLJ14399 (FLJ14399), mRNA
NM_032779	Homo sapiens hypothetical protein FLJ14397 (FLJ14397), mRNA
NM_032778	Homo sapiens hypothetical protein FLJ14393 (FLJ14393), mRNA
NM_032775	Homo sapiens hypothetical protein FLJ14360 (FLJ14360), mRNA
NM_032773	Homo sapiens hypothetical protein MGC4126 (MGC4126), mRNA
NM_032772	Homo sapiens hypothetical protein MGC2555 (MGC2555), mRNA
NM_032771	Homo sapiens hypothetical protein MGC12217 (MGC12217), mRNA
NM_032770	Homo sapiens hypothetical protein MGC16291 (MGC16291), mRNA
NM_032765	Homo sapiens hypothetical protein MGC16175 (MGC16175), mRNA
NM_032764	Homo sapiens hypothetical protein MGC16153 (MGC16153), mRNA
NM_032762	Homo sapiens hypothetical protein MGC16121 (MGC16121), mRNA
NM_032761	Homo sapiens hypothetical protein MGC16075 (MGC16075), mRNA
NM_032759	Homo sapiens hypothetical protein FLJ11328 (FLJ11328), mRNA
NM_032758	Homo sapiens hypothetical protein MGC1346 (MGC1346), mRNA
NM_032757	Homo sapiens hypothetical protein MGC15705 (MGC15705), mRNA
NM_032755	Homo sapiens hypothetical protein MGC15634 (MGC15634), mRNA
NM_032751	Homo sapiens hypothetical protein MGC15504 (MGC15504), mRNA
NM_032750	Homo sapiens hypothetical protein MGC15429 (MGC15429), mRNA
NM_032747	Homo sapiens hypothetical protein MGC14697 (MGC14697), mRNA
NM_032746	Homo sapiens hypothetical protein MGC12538 (MGC12538), mRNA
NM_032740	Homo sapiens hypothetical protein MGC5391 (MGC5391), mRNA
NM_032739	Homo sapiens hypothetical protein MGC5370 (MGC5370), mRNA
NM_032735	Homo sapiens hypothetical protein MGC13168 (MGC13168), mRNA
NM_032733	Homo sapiens hypothetical protein MGC12679 (MGC12679), mRNA
NM_032732	Homo sapiens hypothetical protein MGC10763 (MGC10763), mRNA
NM_032731	Homo sapiens hypothetical protein MGC14353 (MGC14353), mRNA
NM_032730	Homo sapiens NOGO-interacting mitochondrial protein (NIMP), mRNA
NM_032727	Homo sapiens internexin neuronal intermediate filament protein, alpha (INA), mRNA
NM_032726	Homo sapiens hypothetical protein MGC12837 (MGC12837), mRNA
NM_032725	Homo sapiens hypothetical protein MGC13125 (MGC13125), mRNA
NM_032724	Homo sapiens hypothetical protein MGC13269 (MGC13269), mRNA
NM_032722	Homo sapiens hypothetical protein MGC13275 (MGC13275), mRNA
NM_032721	Homo sapiens hypothetical protein MGC11314 (MGC11314), mRNA
NM_032718	Homo sapiens hypothetical protein MGC11332 (MGC11332), mRNA

NM_032717	Homo sapiens hypothetical protein MGC11324 (MGC11324), mRNA
NM_032714	Homo sapiens hypothetical protein MGC13251 (MGC13251), mRNA
NM_032710	Homo sapiens hypothetical protein MGC13053 (MGC13053), mRNA
NM_032709	Homo sapiens hypothetical protein MGC13047 (MGC13047), mRNA
NM_032701	Homo sapiens hypothetical protein MGC2705 (MGC2705), mRNA
NM_032691	Homo sapiens hypothetical protein MGC11082 (MGC11082), mRNA
NM_032690	Homo sapiens hypothetical protein MGC13198 (MGC13198), mRNA
NM_032687	Homo sapiens hypothetical protein MGC13010 (MGC13010), mRNA
NM_032683	Homo sapiens hypothetical protein MGC12972 (MGC12972), mRNA
NM_032680	Homo sapiens hypothetical protein MGC4266 (MGC4266), mRNA
NM_032679	Homo sapiens hypothetical protein MGC4400 (MGC4400), mRNA
NM_032676	Homo sapiens hypothetical protein MGC10955 (MGC10955), mRNA
NM_032673	Homo sapiens hypothetical protein MGC10882 (MGC10882), mRNA
NM_032671	Homo sapiens hypothetical protein MGC10814 (MGC10814), mRNA
NM_032664	Homo sapiens hypothetical protein MGC11141 (MGC11141), mRNA
NM_032663	Homo sapiens hypothetical protein MGC10702 (MGC10702), mRNA
NM_032658	Homo sapiens hypothetical protein MGC10701 (MGC10701), mRNA
NM_032654	Homo sapiens hypothetical protein MGC10981 (MGC10981), mRNA
NM_032653	Homo sapiens hypothetical protein MGC10960 (MGC10960), mRNA
NM_032648	Homo sapiens hypothetical protein MGC10820 (MGC10820), mRNA
NM_032647	Homo sapiens hypothetical protein MGC10561 (MGC10561), mRNA
NM_032644	Homo sapiens hypothetical protein MGC2452 (MGC2452), mRNA
NM_032641	Homo sapiens hypothetical protein MGC2519 (MGC2519), mRNA
NM_032638	Homo sapiens hypothetical protein MGC2306 (MGC2306), mRNA
NM_032633	Homo sapiens hypothetical protein MGC5457 (MGC5457), mRNA
NM_032632	Homo sapiens hypothetical protein MGC5378 (MGC5378), mRNA
NM_032630	Homo sapiens HeLa cyclin-dependent kinase 2 interacting protein (CINP), mRNA
NM_032627	Homo sapiens hypothetical protein MGC3181 (MGC3181), mRNA
NM_032626	Homo sapiens hypothetical brain protein my038 (MY038), mRNA
NM_032624	Homo sapiens hypothetical brain protein my050 (MY050), mRNA
NM_032623	Homo sapiens ovary-specific acidic protein (OSAP), mRNA
NM_032622	Homo sapiens multi-PDZ-domain-containing protein (LNX), mRNA
NM_032620	Homo sapiens mitochondrial GTP binding protein (GTPBG3), mRNA
NM_018622	Homo sapiens presenilins associated rhomboid-like protein (PARL), mRNA
NM_032498	Homo sapiens homeobox protein from AL590526 (LOC84528), mRNA
NM_032600	Homo sapiens testes development-related NYD-SP17 (NYD-SP17), mRNA
NM_032599	Homo sapiens testes development-related NYD-SP18 (NYD-SP18), mRNA
NM_032594	Homo sapiens insulinoma-associated protein IA-6 (INSM2), mRNA
NM_032585	Homo sapiens testis-specific transcript, Y-linked 6 (TTTY6), mRNA
NM_032575	Homo sapiens Kruppel-like zinc finger protein GLIS2 (GLIS2), mRNA
NM_032573	Homo sapiens testis-specific protein TSP-NY (TSP-NY), mRNA
NM_032572	Homo sapiens ribonuclease 7 (RNASE7), mRNA
NM_032568	Homo sapiens GABA(A) receptors associated protein like 3 (GABARAPL3), mRNA
NM_032567	Homo sapiens testis-specific protein NYD-TSP1 (NYD-TSP1), mRNA
NM_032566	Homo sapiens esophagus cancer-related gene-2 (ECG2), mRNA
NM_032562	Homo sapiens group XIII secreted phospholipase A2 (PLA2G13), mRNA
NM_032547	Homo sapiens short coiled-coil protein (HRIHFB2072), mRNA
NM_032546	Homo sapiens ring finger protein 30 (RNF30), mRNA
NM_032519	Homo sapiens hypothetical protein HT023 (HT023), mRNA
NM_032513	Homo sapiens hypothetical protein MGC11303 similar to Zink transporter 2

	(MGC11303), mRNA
NM_032490	Homo sapiens PNAS-127 protein (PNAS-127), mRNA
NM_032488	Homo sapiens protein related with psoriasis (LOC84518), mRNA
NM_032471	Homo sapiens protein kinase (cAMP-dependent, catalytic) inhibitor beta (PKIB), mRNA
NM_032292	Homo sapiens hypothetical protein FLJ20203 (FLJ20203), mRNA
NM_032263	Homo sapiens hypothetical protein DKFZp434B227 (DKFZp434B227), mRNA
NM_015178	Homo sapiens KIAA0717 protein (KIAA0717), mRNA
NM_032410	Homo sapiens hook3 protein (HOOK3), mRNA
NM_032108	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (SEMA6B), mRNA
NM_015636	Homo sapiens DKFZP586J0119 protein (DKFZP586J0119), mRNA
NM_015701	Homo sapiens hypothetical protein (CL25084), mRNA
NM_015224	Homo sapiens KIAA1105 protein (RAP140), mRNA
NM_032390	Homo sapiens nucleolar protein interacting with the FHA domain of pKi-67 (NIFK), mRNA
NM_032388	Homo sapiens nasopharyngeal carcinoma-related protein (NPCR), mRNA
NM_032383	Homo sapiens Hermansky-Pudlak syndrome 3 (HPS3), mRNA
NM_032378	Homo sapiens hypothetical protein FLJ20897 (FLJ20897), mRNA
NM_032376	Homo sapiens hypothetical protein MGC4251 (MGC4251), mRNA
NM_032375	Homo sapiens hypothetical protein MGC2865 (MGC2865), mRNA
NM_032373	Homo sapiens hypothetical protein MGC16202 (MGC16202), mRNA
NM_032370	Homo sapiens hypothetical protein MGC15716 (MGC15716), mRNA
NM_032369	Homo sapiens hypothetical protein MGC15619 (MGC15619), mRNA
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NM_032336	Homo sapiens hypothetical protein MGC14799 (MGC14799), mRNA
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NM_032328	Homo sapiens hypothetical protein MGC12458 (MGC12458), mRNA
NM_032322	Homo sapiens hypothetical protein MGC13061 (MGC13061), mRNA
NM_032321	Homo sapiens hypothetical protein MGC13057 (MGC13057), mRNA
NM_032319	Homo sapiens chromosome 2 open reading frame 7 (C2orf7), mRNA

NM_032315	Homo sapiens hypothetical protein MGC4399 (MGC4399), mRNA
NM_032314	Homo sapiens hypothetical protein MGC4767 (MGC4767), mRNA
NM_032313	Homo sapiens hypothetical protein MGC3232 (MGC3232), mRNA
NM_032312	Homo sapiens hypothetical protein MGC11061 (MGC11061), mRNA
NM_032310	Homo sapiens hypothetical protein MGC11115 (MGC11115), mRNA
NM_032307	Homo sapiens hypothetical protein MGC10999 (MGC10999), mRNA
NM_032303	Homo sapiens hypothetical protein MGC10940 (MGC10940), mRNA
NM_032302	Homo sapiens hypothetical protein MGC10911 (MGC10911), mRNA
NM_032301	Homo sapiens hypothetical protein MGC10870 (MGC10870), mRNA
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NM_032297	Homo sapiens hypothetical protein DKFZp761D112 (DKFZp761D112), mRNA
NM_032296	Homo sapiens hypothetical protein DKFZp761A132 (DKFZp761A132), mRNA
NM_032295	Homo sapiens hypothetical protein DKFZp761N0624 (DKFZp761N0624), mRNA
NM_032294	Homo sapiens hypothetical protein DKFZp761M0423 (DKFZp761M0423), mRNA
NM_032289	Homo sapiens hypothetical protein DKFZp761B0514 (DKFZp761B0514), mRNA
NM_032287	Homo sapiens hypothetical protein DKFZp761O17121 (DKFZp761O17121), mRNA
NM_032280	Homo sapiens hypothetical protein DKFZp761J139 (DKFZp761J139), mRNA
NM_032278	Homo sapiens hypothetical protein DKFZp547P082 (DKFZp547P082), mRNA
NM_032274	Homo sapiens hypothetical protein DKFZp547F072 (DKFZp547F072), mRNA
NM_032271	Homo sapiens hypothetical protein DKFZp586I021 (DKFZp586I021), mRNA
NM_032270	Homo sapiens hypothetical protein DKFZp586J1119 (DKFZp586J1119), mRNA
NM_032269	Homo sapiens hypothetical protein DKFZp434I099 (DKFZp434I099), mRNA
NM_032266	Homo sapiens hypothetical protein DKFZp434G118 (DKFZp434G118), mRNA
NM_032265	Homo sapiens hypothetical protein DKFZp434N127 (DKFZp434N127), mRNA
NM_032262	Homo sapiens hypothetical protein DKFZp434N035 (DKFZp434N035), mRNA
NM_032257	Homo sapiens hypothetical protein DKFZp434N2435 (DKFZp434N2435), mRNA
NM_032256	Homo sapiens hypothetical protein DKFZp434K2435 (DKFZp434K2435), mRNA
NM_032255	Homo sapiens hypothetical protein DKFZp434I1930 (DKFZp434I1930), mRNA
NM_032254	Homo sapiens hypothetical protein DKFZp434F142 (DKFZp434F142), mRNA
NM_032247	Homo sapiens hypothetical protein DKFZp434E0519 (DKFZp434E0519), mRNA
NM_032242	Homo sapiens hypothetical protein DKFZp564A176 (DKFZp564A176), mRNA
NM_032238	Homo sapiens hypothetical protein FLJ23416 (FLJ23416), mRNA
NM_032235	Homo sapiens hypothetical protein FLJ23138 (FLJ23138), mRNA
NM_032234	Homo sapiens hypothetical protein FLJ23059 (FLJ23059), mRNA
NM_032233	Homo sapiens hypothetical protein FLJ23027 (FLJ23027), mRNA
NM_032229	Homo sapiens hypothetical protein FLJ22774 (FLJ22774), mRNA
NM_032221	Homo sapiens hypothetical protein FLJ22369 (FLJ22369), mRNA
NM_032213	Homo sapiens hypothetical protein FLJ21977 (FLJ21977), mRNA
NM_032212	Homo sapiens similar to DNA-directed RNA polymerase I (135 kDa) (Rpo1-2), mRNA
NM_032207	Homo sapiens hypothetical protein FLJ21742 (FLJ21742), mRNA
NM_032205	Homo sapiens hypothetical protein FLJ21615 (FLJ21615), mRNA
NM_032196	Homo sapiens hypothetical protein KIAA1259 (KIAA1259), mRNA
NM_032192	Homo sapiens hypothetical protein FLJ20940 (FLJ20940), mRNA

NM_032191	Homo sapiens hypothetical protein FLJ14326 (FLJ14326), mRNA
NM_032187	Homo sapiens hypothetical protein FLJ14026 (FLJ14026), mRNA
NM_032186	Homo sapiens hypothetical protein FLJ13964 (FLJ13964), mRNA
NM_032181	Homo sapiens hypothetical protein FLJ13391 (FLJ13391), mRNA
NM_032179	Homo sapiens hypothetical protein FLJ20542 (FLJ20542), mRNA
NM_032178	Homo sapiens hypothetical protein FLJ13291 (FLJ13291), mRNA
NM_032175	Homo sapiens hypothetical protein FLJ12787 (FLJ12787), mRNA
NM_032174	Homo sapiens hypothetical protein FLJ12770 (FLJ12770), mRNA
NM_032169	Homo sapiens hypothetical protein FLJ12592 (FLJ12592), mRNA
NM_032164	Homo sapiens hypothetical protein FLJ12298 (FLJ12298), mRNA
NM_032162	Homo sapiens hypothetical protein FLJ11952 (FLJ11952), mRNA
NM_032155	Homo sapiens hypothetical protein DKFZp547I094 (DKFZp547I094), mRNA
NM_032152	Homo sapiens PRAM-1 protein (PRAM-1), mRNA
NM_032149	Homo sapiens hypothetical protein DKFZp434G072 (DKFZP434G072), mRNA
NM_032147	Homo sapiens hypothetical protein DKFZp434D0127 (DKFZP434D0127), mRNA
NM_032146	Homo sapiens hypothetical protein DKFZp434L1123 similar to mouse Arl6 (DKFZP434L1123), mRNA
NM_032143	Homo sapiens hypothetical protein DKFZp434B1727 (DKFZP434B1727), mRNA
NM_032142	Homo sapiens hypothetical protein FLJ10352 (FLJ10352), mRNA
NM_032141	Homo sapiens hypothetical protein DKFZp434K1421 (DKFZP434K1421), mRNA
NM_032140	Homo sapiens hypothetical protein DKFZp434A1319 (DKFZP434A1319), mRNA
NM_032135	Homo sapiens hypothetical protein DKFZp434F1017 (DKFZP434F1017), mRNA
NM_032134	Homo sapiens hypothetical protein DKFZp434P0316 (DKFZP434P0316), mRNA
NM_032131	Homo sapiens hypothetical protein DKFZp434P0714 (DKFZP434P0714), mRNA
NM_032130	Homo sapiens hypothetical protein DKFZp434J0113 (DKFZP434J0113), mRNA
NM_032129	Homo sapiens hypothetical protein DKFZp434H2010 (DKFZP434H2010), mRNA
NM_032128	Homo sapiens hypothetical protein DKFZp566M114 (DKFZP566M114), mRNA
NM_032127	Homo sapiens hypothetical protein DKFZp566M1046 (DKFZP566M1046), mRNA
NM_032126	Homo sapiens hypothetical protein DKFZp564J047 (DKFZP564J047), mRNA
NM_032124	Homo sapiens hypothetical protein DKFZp564D1378 (DKFZP564D1378), mRNA
NM_032121	Homo sapiens hypothetical protein DKFZp564K142 similar to implantation-associated protein (DKFZp564K142), mRNA
NM_032118	Homo sapiens hypothetical protein FLJ12953 similar to Mus musculus D3Mm3e (FLJ12953), mRNA
NM_032117	Homo sapiens GAJ protein (GAJ), mRNA
NM_032116	Homo sapiens hypothetical protein MGC2599 similar to katanin p60 subunit A 1 2599 (MGC2599), mRNA
NM_032112	Homo sapiens mitochondrial ribosomal protein L43 (MRPL43), mRNA
NM_020898	Homo sapiens KIAA1536 protein (KIAA1536), mRNA
NM_020726	Homo sapiens neurolysin (metallopeptidase M3 family) (NLN), mRNA
NM_020707	Homo sapiens KIAA1173 protein (KIAA1173), mRNA
NM_018670	Homo sapiens hypothetical protein (IR1899308), mRNA

NM_018385	Homo sapiens hypothetical protein FLJ11301 (FLJ11301), mRNA
NM_018064	Homo sapiens hypothetical protein FLJ10342 (FLJ10342), mRNA
NM_017607	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12C (PPP1R12C), mRNA
NM_015645	Homo sapiens DKFZP586B0621 protein (CTRP5), mRNA
NM_015528	Homo sapiens DKFZP566H073 protein (DKFZP566H073), mRNA
NM_015512	Homo sapiens DKFZP434A236 protein (DKFZP434A236), mRNA
NM_015426	Homo sapiens DKFZP434C245 protein (DKFZP434C245), mRNA
NM_015292	Homo sapiens KIAA0747 protein (KIAA0747), mRNA
NM_015236	Homo sapiens KIAA0768 protein (LEC3), mRNA
NM_015196	Homo sapiens KIAA0922 protein (KIAA0922), mRNA
NM_015112	Homo sapiens KIAA0807 protein (MAST205), mRNA
NM_015070	Homo sapiens KIAA0853 protein (KIAA0853), mRNA
NM_032308	Homo sapiens hypothetical protein MGC4189 (MGC4189), mRNA
NM_004801	Homo sapiens neurexin 1 (NRXN1), mRNA
NM_001221	Homo sapiens calcium/calmodulin-dependent protein kinase (CaM kinase) II delta (CAMK2D), mRNA
NM_015208	Homo sapiens KIAA0874 protein (KIAA0874), mRNA
NM_032043	Homo sapiens BRCA1-interacting protein 1 (BRIP1), mRNA
NM_032040	Homo sapiens hypothetical protein DKFZp564K0322 (DKFZP564K0322), mRNA
NM_032037	Homo sapiens serine/threonine protein kinase SSTK (SSTK), mRNA
NM_032033	Homo sapiens FKSG43 (FKSG43), mRNA
NM_032032	Homo sapiens FKSG42 (FKSG42), mRNA
NM_032031	Homo sapiens FKSG17 (FKSG17), mRNA
NM_032029	Homo sapiens FKSG87 protein (FKSG87), mRNA
NM_032026	Homo sapiens CDA11 protein (CDA11), mRNA
NM_032024	Homo sapiens CDA017 protein (CDA017), mRNA
NM_032023	Homo sapiens AD037 protein (AD037), mRNA
NM_032022	Homo sapiens AD036 protein (AD036), mRNA
NM_031956	Homo sapiens NYD-SP14 protein (NYD-SP14), mRNA
NM_031954	Homo sapiens MSTP028 protein (MSTP028), mRNA
NM_031953	Homo sapiens MSTP043 protein (MSTP043), mRNA
NM_031936	Homo sapiens G protein-coupled receptor 61 (GPR61), mRNA
NM_031934	Homo sapiens RAB34, member RAS oncogene family (RAB34), mRNA
NM_031933	Homo sapiens wingless-type MMTV integration site family, member 8A (WNT8A), transcript variant 1, mRNA
NM_031932	Homo sapiens testis transcript Y 14 (TTY14), mRNA
NM_031931	Homo sapiens testis transcript Y 13 (TTY13), mRNA
NM_031930	Homo sapiens testis transcript Y 12 (TTY12), mRNA
NM_031929	Homo sapiens testis transcript Y 11 (TTY11), mRNA
NM_031927	Homo sapiens testis transcript Y 9 (TTY9), mRNA
NM_031926	Homo sapiens testis transcript Y 7 (TTY7), mRNA
NM_031925	Homo sapiens transmembrane protein induced by tumor necrosis factor alpha (TMPIT), mRNA
NM_031924	Homo sapiens radial spoke protein 3 (RSP3), mRNA
NM_031917	Homo sapiens angiopoietin-related protein 5 (ARP5), mRNA
NM_031948	Homo sapiens marapsin (MPN), mRNA
NM_031908	Homo sapiens complement-c1q tumor necrosis factor-related protein 2 (CTRP2), mRNA
NM_031905	Homo sapiens hypothetical protein MGC3195 (MGC3195), mRNA
NM_031889	Homo sapiens enamelin (ENAM), mRNA

NM_022447	Homo sapiens topoisomerase-related function protein 4-2 (TRF4-2), mRNA
NM_031485	Homo sapiens glutamate rich WD repeat protein GRWD (GRWD), mRNA
NM_031484	Homo sapiens hypothetical protein MGC4415 (MGC4415), mRNA
NM_031479	Homo sapiens hypothetical protein MGC4638 (MGC4638), mRNA
NM_031474	Homo sapiens hypothetical protein DKFZp761G1913 (DKFZP761G1913), mRNA
NM_031466	Homo sapiens KIAA1882 protein (MGC4737), mRNA
NM_031465	Homo sapiens hypothetical protein MGC13204 (MGC13204), mRNA
NM_031464	Homo sapiens hypothetical protein MGC11287 similar to ribosomal protein S6 kinase , (MGC11287), mRNA
NM_031459	Homo sapiens sestrin 2 (SES2), mRNA
NM_031455	Homo sapiens hypothetical protein DKFZp761F241 (DKFZP761F241), mRNA
NM_031453	Homo sapiens hypothetical protein MGC11034 (MGC11034), mRNA
NM_031452	Homo sapiens hypothetical protein MGC2560 (MGC2560), mRNA
NM_031449	Homo sapiens KIAA1886 protein (DKFZP761I2123), mRNA
NM_031447	Homo sapiens hypothetical protein MGC13033 (MGC13033), mRNA
NM_031446	Homo sapiens hypothetical protein PNAS-131 (PNAS-131), mRNA
NM_031437	Homo sapiens hypothetical protein MGC10823 (MGC10823), mRNA
NM_031436	Homo sapiens hypothetical protein MGC10612 (MGC10612), mRNA
NM_031435	Homo sapiens hypothetical protein DKFZp564I0422 (DKFZP564I0422), mRNA
NM_031430	Homo sapiens rab interacting lysosomal protein (RILP), mRNA
NM_031425	Homo sapiens hypothetical protein MGC10812 (MGC10812), mRNA
NM_031423	Homo sapiens hypothetical protein NUF2R (NUF2R), mRNA
NM_031421	Homo sapiens hypothetical protein DKFZp434H0115 (DKFZP434H0115), mRNA
NM_031412	Homo sapiens GABA(A) receptor-associated protein like 1 (GABARAPL1), mRNA
NM_004637	Homo sapiens RAB7, member RAS oncogene family (RAB7), mRNA
NM_031283	Homo sapiens HMG-box transcription factor TCF-3 (TCF-3), mRNA
NM_031307	Homo sapiens hypothetical protein FKSG32 (FKSG32), mRNA
NM_031305	Homo sapiens hypothetical protein DKFZp564B1162 (DKFZP564B1162), mRNA
NM_031301	Homo sapiens hypothetical protein DKFZp564D0372 (DKFZP564D0372), mRNA
NM_031298	Homo sapiens hypothetical protein MGC2963 (MGC2963), mRNA
NM_031293	Homo sapiens hypothetical protein DKFZp434G131 (DKFZP434G131), mRNA
NM_031292	Homo sapiens hypothetical protein DKFZp434G1415 (DKFZP434G1415), mRNA
NM_031288	Homo sapiens PAP-1 binding protein (PAPA-1), mRNA
NM_031284	Homo sapiens hypothetical protein DKFZp434B195 (DKFZP434B195), mRNA
NM_030972	Homo sapiens hypothetical protein MGC5384 (MGC5384), mRNA
NM_030901	Homo sapiens olfactory receptor, family 7, subfamily A, member 17 (OR7A17), mRNA
NM_017990	Homo sapiens hypothetical protein FLJ10079 (FLJ10079), mRNA
NM_031219	Homo sapiens hypothetical protein MGC12904 (MGC12904), mRNA
NM_031218	Homo sapiens hypothetical protein FLJ12488 (FLJ12488), mRNA
NM_031214	Homo sapiens hypothetical protein AF311304 (AF311304), mRNA
NM_031210	Homo sapiens hypothetical protein DC50 (DC50), mRNA
NM_031207	Homo sapiens hypothetical protein HT036 (HT036), mRNA
NM_007013	Homo sapiens WW domain-containing protein 1 (WWP1), mRNA
NM_030897	Homo sapiens hypothetical protein FLJ21617 (FLJ21617), mRNA
NM_030978	Homo sapiens hypothetical protein similar to actin related protein 2/3 complex,

	subunit 5 (MGC3038), mRNA
NM_030971	Homo sapiens similar to rat tricarboxylate carrier-like protein (BA108L7.2), mRNA
NM_030965	Homo sapiens similar to sialyltransferase 7 ((alpha-N-acetylneuraminyl 2,3-betagalactosyl-1,3)-N-acetyl galactosaminide alpha-2,6-sialyltransferase) E (MGC3184), mRNA
NM_030960	Homo sapiens sperm acrosome associated 1 (SPACA1), mRNA
NM_030958	Homo sapiens organic anion transporter polypeptide-related protein 4 (OATPRP4), mRNA
NM_030952	Homo sapiens hypothetical protein DKFZp434J037 (DKFZP434J037), mRNA
NM_030940	Homo sapiens hypothetical protein MGC4276 similar to CG8198 (MGC4276), mRNA
NM_030937	Homo sapiens hypothetical protein hCLA-iso (HCLA-ISO), mRNA
NM_030929	Homo sapiens hypothetical protein FKSG28 (FKSG28), mRNA
NM_030921	Homo sapiens hypothetical protein DC42 (DC42), mRNA
NM_030917	Homo sapiens hypothetical protein DKFZp586K0717 (DKFZP586K0717), mRNA
NM_030915	Homo sapiens hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA
NM_030914	Homo sapiens hypothetical protein MGC2668 (MGC2668), mRNA
NM_030907	Homo sapiens hypothetical protein MGC10731 (MGC10731), mRNA
NM_030895	Homo sapiens hypothetical protein FLJ14129 (FLJ14129), mRNA
NM_030891	Homo sapiens leucine-rich repeat-containing 3 (LRRC3), mRNA
NM_030755	Homo sapiens thioredoxin domain-containing (TXNDC), mRNA
NM_030819	Homo sapiens hypothetical protein MGC11335 (MGC11335), mRNA
NM_030814	Homo sapiens hypothetical protein GL012 (GL012), mRNA
NM_030810	Homo sapiens hypothetical protein MGC3178 (MGC3178), mRNA
NM_030804	Homo sapiens hypothetical protein DKFZp434E2135 (DKFZP434E2135), mRNA
NM_030794	Homo sapiens hypothetical protein FLJ21007 (FLJ21007), mRNA
NM_030759	Homo sapiens nuclear receptor binding factor-2 (NRBF-2), mRNA
NM_030795	Homo sapiens stathmin-like 4 (STMN4), mRNA
NM_020909	Homo sapiens KIAA1548 protein (KIAA1548), mRNA
NM_018023	Homo sapiens hypothetical protein FLJ10201 (FLJ10201), mRNA
NM_023009	Homo sapiens macrophage myristoylated alanine-rich C kinase substrate (MACMARCKS), mRNA
NM_025230	Homo sapiens hypthetical protein PRO2389 (PRO2389), mRNA
NM_025222	Homo sapiens hypothetical protein PRO2730 (PRO2730), mRNA
NM_025170	Homo sapiens hypothetical protein FLJ12987 (FLJ12987), mRNA
NM_024681	Homo sapiens hypothetical protein FLJ12242 (FLJ12242), mRNA
NM_024928	Homo sapiens hypothetical protein FLJ22559 (FLJ22559), mRNA
NM_017578	Homo sapiens AKAP-binding sperm protein ropporin (DKFZp434B1222), mRNA
NM_030642	Homo sapiens apolipoprotein L, 5 (APOL5), mRNA
NM_024513	Homo sapiens FYVE and coiled-coil domain containing 1 (FYCO1), mRNA
NM_030621	Homo sapiens helicase-moi (KIAA0928), mRNA
NM_030641	Homo sapiens apolipoprotein L, 6 (APOL6), mRNA
NM_025190	Homo sapiens KIAA1641 protein (KIAA1641), mRNA
NM_025040	Homo sapiens hypothetical protein FLJ21941 (FLJ21941), mRNA
NM_030613	Homo sapiens hypothetical protein FLJ21628 (FLJ21628), mRNA
NM_024820	Homo sapiens KIAA1608 protein (KIAA1608), mRNA
NM_018015	Homo sapiens hypothetical protein FLJ10178 (FLJ10178), mRNA
NM_024762	Homo sapiens hypothetical protein FLJ21603 (FLJ21603), mRNA

NM_024329	Homo sapiens hypothetical protein MGC4342 (MGC4342), mRNA
NM_024087	Homo sapiens DKFZP564L0862 protein (DKFZP564L0862), mRNA
NM_030594	Homo sapiens cytoplasmic polyadenylation element binding protein (CPEB1), mRNA
NM_025084	Homo sapiens hypothetical protein FLJ22795 (FLJ22795), mRNA
NM_025090	Homo sapiens KIAA1453 protein (KIAA1453), mRNA
NM_024939	Homo sapiens hypothetical protein FLJ21918 (FLJ21918), mRNA
NM_024903	Homo sapiens hypothetical protein FLJ14297 (FLJ14297), mRNA
NM_024793	Homo sapiens KIAA0643 protein (KIAA0643), mRNA
NM_024718	Homo sapiens hypothetical protein FLJ10101 (FLJ10101), mRNA
NM_015652	Homo sapiens DKFZP564P1916 protein (DKFZP564P1916), mRNA
NM_025189	Homo sapiens hypothetical protein FLJ13659 (FLJ13659), mRNA
NM_025021	Homo sapiens KIAA0616 protein (KIAA0616), mRNA
NM_025010	Homo sapiens KIAA0795 protein (KIAA0795), mRNA
NM_024894	Homo sapiens hypothetical protein FLJ14075 (FLJ14075), mRNA
NM_024840	Homo sapiens hypothetical protein FLJ13590 (FLJ13590), mRNA
NM_022782	Homo sapiens M-phase phosphoprotein 9 (MPHOSPH9), mRNA
NM_017558	Homo sapiens hypothetical protein DKFZp434L0850 (DKFZp434L0850), mRNA
NM_030580	Homo sapiens hypothetical protein MGC10520 (MGC10520), mRNA
NM_025195	Homo sapiens phosphoprotein regulated by mitogenic pathways (C8FW), mRNA
NM_030581	Homo sapiens hypothetical protein FLJ12270 (FLJ12270), mRNA
NM_030577	Homo sapiens hypothetical protein MGC10993 (MGC10993), mRNA
NM_030576	Homo sapiens hypothetical protein MGC10986 (MGC10986), mRNA
NM_030575	Homo sapiens hypothetical protein MGC10334 (MGC10334), mRNA
NM_030572	Homo sapiens hypothetical protein MGC10946 (MGC10946), mRNA
NM_030571	Homo sapiens hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5 (MGC10924), mRNA
NM_030569	Homo sapiens hypothetical protein MGC10848 (MGC10848), mRNA
NM_030568	Homo sapiens hypothetical protein MGC10818 (MGC10818), mRNA
NM_030567	Homo sapiens hypothetical protein MGC10772 (MGC10772), mRNA
NM_025164	Homo sapiens KIAA0999 protein (KIAA0999), mRNA
NM_025132	Homo sapiens KIAA1638 protein (KIAA1638), mRNA
NM_024668	Homo sapiens hypothetical protein FLJ20288 (FLJ20288), mRNA
NM_024547	Homo sapiens KIAA0467 protein (KIAA0467), mRNA
NM_018418	Homo sapiens hypothetical protein (HSD-3.1), mRNA
NM_025182	Homo sapiens hypothetical protein FLJ11560 (FLJ11560), mRNA
NM_025168	Homo sapiens LAP (leucine-rich repeats and PDZ) and no PDZ protein (LANO), mRNA
NM_025081	Homo sapiens KIAA1305 protein (KIAA1305), mRNA
NM_024750	Homo sapiens leucine-rich repeat-containing 2 (LRRC2), mRNA
NM_025266	Homo sapiens hypothetical protein MGC2780 (MGC2780), mRNA
NM_025265	Homo sapiens hypothetical protein MGC2776 (MGC2776), mRNA
NM_025264	Homo sapiens hypothetical protein MGC2454 (MGC2454), mRNA
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NM_025246	Homo sapiens hypothetical protein MGC3295 (MGC3295), mRNA
NM_025234	Homo sapiens recombination protein REC14 (REC14), mRNA
NM_025221	Homo sapiens calsenilin-like protein (CALP), mRNA
NM_025207	Homo sapiens hypothetical protein PP591 (PP591), mRNA
NM_025204	Homo sapiens hypothetical protein PP2447 (PP2447), mRNA
NM_025203	Homo sapiens hypothetical protein FLJ21945 (FLJ21945), mRNA
NM_025199	Homo sapiens hypothetical protein FLJ20886 (FLJ20886), mRNA

NM_025197	Homo sapiens hypothetical protein FLJ13660 similar to CDK5 activator-binding protein C53 (FLJ13660), mRNA
NM_025187	Homo sapiens hypothetical protein FLJ12076 (FLJ12076), mRNA
NM_025184	Homo sapiens hypothetical protein FLJ22843 (FLJ22843), mRNA
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NM_025104	Homo sapiens hypothetical protein FLJ13087 (FLJ13087), mRNA
NM_025103	Homo sapiens capillary morphogenesis protein 1 (CMG1), mRNA
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NM_025023	Homo sapiens hypothetical protein FLJ14069 (FLJ14069), mRNA
NM_025019	Homo sapiens likely ortholog of mouse tubulin alpha 4 (FLJ13940), mRNA
NM_025012	Homo sapiens hypothetical protein FLJ13769 (FLJ13769), mRNA
NM_025009	Homo sapiens hypothetical protein FLJ13621 (FLJ13621), mRNA
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NM_024940	Homo sapiens hypothetical protein FLJ21034 (FLJ21034), mRNA
NM_024937	Homo sapiens hypothetical protein FLJ12929 (FLJ12929), mRNA
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NM_024912	Homo sapiens hypothetical protein FLJ14327 (FLJ14327), mRNA
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NM_024866	Homo sapiens hypothetical protein FLJ21135 (FLJ21135), mRNA
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NM_024846	Homo sapiens hypothetical protein FLJ11710 (FLJ11710), mRNA
NM_024845	Homo sapiens hypothetical protein FLJ14154 (FLJ14154), mRNA
NM_024844	Homo sapiens hypothetical protein FLJ12549 (FLJ12549), mRNA
NM_024843	Homo sapiens duodenal cytochrome b (FLJ23462), mRNA
NM_024838	Homo sapiens hypothetical protein FLJ22002 (FLJ22002), mRNA
NM_024834	Homo sapiens hypothetical protein FLJ13081 (FLJ13081), mRNA
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NM_024733	Homo sapiens hypothetical protein FLJ14345 (FLJ14345), mRNA
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NM_024724	Homo sapiens hypothetical protein FLJ22332 (FLJ22332), mRNA
NM_024721	Homo sapiens likely ortholog of mouse zinc finger homeodomain 4 (FLJ20980), mRNA
NM_024713	Homo sapiens hypothetical protein FLJ22557 (FLJ22557), mRNA
NM_024712	Homo sapiens engulfment and cell motility 3 (ced-12 homolog, C. elegans) (ELMO3), mRNA
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NM_024614	Homo sapiens hypothetical protein FLJ13197 (FLJ13197), mRNA
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NM_024608	Homo sapiens hypothetical protein FLJ22402 (FLJ22402), mRNA

NM_024607	Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA
NM_024604	Homo sapiens hypothetical protein FLJ21908 (FLJ21908), mRNA
NM_024603	Homo sapiens hypothetical protein FLJ11588 (FLJ11588), mRNA
NM_024599	Homo sapiens hypothetical protein FLJ22341 (FLJ22341), mRNA
NM_024598	Homo sapiens hypothetical protein FLJ13154 (FLJ13154), mRNA
NM_024597	Homo sapiens hypothetical protein FLJ12649 (FLJ12649), mRNA
NM_024596	Homo sapiens hypothetical protein FLJ12847 (FLJ12847), mRNA
NM_024594	Homo sapiens hypothetical protein FLJ12899 (FLJ12899), mRNA
NM_024593	Homo sapiens hypothetical protein FLJ11767 (FLJ11767), mRNA
NM_024592	Homo sapiens hypothetical protein FLJ13352 (FLJ13352), mRNA
NM_024590	Homo sapiens hypothetical protein FLJ23548 (FLJ23548), mRNA
NM_024589	Homo sapiens hypothetical protein FLJ22386 (FLJ22386), mRNA
NM_024588	Homo sapiens hypothetical protein FLJ23584 (FLJ23584), mRNA
NM_024587	Homo sapiens hypothetical protein FLJ22353 (FLJ22353), mRNA
NM_024583	Homo sapiens hypothetical protein FLJ23142 (FLJ23142), mRNA
NM_024582	Homo sapiens hypothetical protein FLJ23056 (FLJ23056), mRNA
NM_024581	Homo sapiens hypothetical protein FLJ13942 (FLJ13942), mRNA
NM_024579	Homo sapiens hypothetical protein FLJ23221 (FLJ23221), mRNA
NM_024578	Homo sapiens hypothetical protein FLJ22709 (FLJ22709), mRNA
NM_024577	Homo sapiens hypothetical protein FLJ13605 (FLJ13605), mRNA
NM_024576	Homo sapiens hypothetical protein FLJ21079 (FLJ21079), mRNA
NM_024575	Homo sapiens hypothetical protein FLJ23467 (FLJ23467), mRNA
NM_024574	Homo sapiens hypothetical protein FLJ23191 (FLJ23191), mRNA
NM_024573	Homo sapiens hypothetical protein FLJ12910 (FLJ12910), mRNA
NM_024572	Homo sapiens hypothetical protein FLJ12691 (FLJ12691), mRNA
NM_024569	Homo sapiens hypothetical protein FLJ21047 (FLJ21047), mRNA
NM_024567	Homo sapiens hypothetical protein FLJ21616 (FLJ21616), mRNA
NM_024564	Homo sapiens hypothetical protein FLJ11715 (FLJ11715), mRNA
NM_024563	Homo sapiens hypothetical protein FLJ14054 (FLJ14054), mRNA
NM_024560	Homo sapiens hypothetical protein FLJ21963 (FLJ21963), mRNA
NM_024558	Homo sapiens hypothetical protein FLJ13920 (FLJ13920), mRNA
NM_024557	Homo sapiens hypothetical protein FLJ11608 (FLJ11608), mRNA
NM_024554	Homo sapiens hypothetical protein FLJ11413 (FLJ11413), mRNA
NM_024548	Homo sapiens hypothetical protein FLJ23047 (FLJ23047), mRNA
NM_024545	Homo sapiens hypothetical protein FLJ12761 (FLJ12761), mRNA
NM_024544	Homo sapiens hypothetical protein FLJ12875 (FLJ12875), mRNA
NM_024541	Homo sapiens hypothetical protein FLJ13114 (FLJ13114), mRNA
NM_024539	Homo sapiens hypothetical protein FLJ23516 (FLJ23516), mRNA
NM_024537	Homo sapiens hypothetical protein FLJ12118 (FLJ12118), mRNA
NM_024536	Homo sapiens hypothetical protein FLJ22678 (FLJ22678), mRNA
NM_024535	Homo sapiens hypothetical protein FLJ22021 (FLJ22021), mRNA
NM_024533	Homo sapiens hypothetical protein FLJ22167 (FLJ22167), mRNA
NM_024531	Homo sapiens hypothetical protein FLJ11856 (FLJ11856), mRNA
NM_024530	Homo sapiens hypothetical protein FLJ23306 (FLJ23306), mRNA
NM_024528	Homo sapiens hypothetical protein FLJ22626 (FLJ22626), mRNA
NM_024527	Homo sapiens hypothetical protein FLJ11743 (FLJ11743), mRNA
NM_024525	Homo sapiens hypothetical protein FLJ22584 (FLJ22584), mRNA
NM_024524	Homo sapiens hypothetical protein FLJ20986 (FLJ20986), mRNA
NM_024521	Homo sapiens hypothetical protein FLJ21459 (FLJ21459), mRNA
NM_024520	Homo sapiens hypothetical protein FLJ22555 (FLJ22555), mRNA

NM_024519	Homo sapiens hypothetical protein FLJ13725 (FLJ13725), mRNA
NM_024509	Homo sapiens hypothetical protein MGC2656 (MGC2656), mRNA
NM_024506	Homo sapiens hypothetical protein MGC10771 (MGC10771), mRNA
NM_022893	Homo sapiens B-cell CLL/lymphoma 11A (zinc finger protein) (BCL11A), mRNA
NM_015113	Homo sapiens KIAA0399 protein (KIAA0399), mRNA
NM_015545	Homo sapiens KIAA0632 protein (KIAA0632), mRNA
NM_020299	Homo sapiens aldo-keto reductase family 1, member B10 (aldose reductase) (AKR1B10), mRNA
NM_003308	Homo sapiens testis specific protein, Y-linked (TSPY), mRNA
NM_024339	Homo sapiens hypothetical protein MGC2655 (MGC2655), mRNA
NM_024334	Homo sapiens hypothetical protein MGC3222 (MGC3222), mRNA
NM_024328	Homo sapiens hypothetical protein MGC2652 (MGC2652), mRNA
NM_024327	Homo sapiens hypothetical protein MGC2508 (MGC2508), mRNA
NM_024323	Homo sapiens hypothetical protein MGC11271 (MGC11271), mRNA
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NM_024320	Homo sapiens hypothetical protein MGC11242 (MGC11242), mRNA
NM_024319	Homo sapiens hypothetical protein MGC4174 (MGC4174), mRNA
NM_024314	Homo sapiens hypothetical protein MGC4294 (MGC4294), mRNA
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NM_024303	Homo sapiens hypothetical protein MGC4161 (MGC4161), mRNA
NM_024297	Homo sapiens hypothetical protein MGC2941 (MGC2941), mRNA
NM_024293	Homo sapiens hypothetical protein MGC3035 (MGC3035), mRNA
NM_023003	Homo sapiens transmembrane 6 superfamily member 1 (TM6SF1), mRNA
NM_015254	Homo sapiens kinesin family member 13B (KIF13B), mRNA
NM_015127	Homo sapiens Mid-1-related chloride channel 1 (KIAA0761), mRNA
NM_024033	Homo sapiens hypothetical protein MGC5242 (MGC5242), mRNA
NM_024122	Homo sapiens hypothetical protein MGC4825 (MGC4825), mRNA
NM_024121	Homo sapiens hypothetical protein FLJ20979 (FLJ20979), mRNA
NM_024119	Homo sapiens hypothetical protein FLJ11354 (FLJ11354), mRNA
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NM_024115	Homo sapiens hypothetical protein MGC4309 (MGC4309), mRNA
NM_024111	Homo sapiens hypothetical protein MGC4504 (MGC4504), mRNA
NM_024109	Homo sapiens hypothetical protein MGC2654 (MGC2654), mRNA
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NM_024106	Homo sapiens hypothetical protein MGC2663 (MGC2663), mRNA
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NM_024097	Homo sapiens hypothetical protein MGC955 (MGC955), mRNA
NM_024094	Homo sapiens hypothetical protein MGC5528 (MGC5528), mRNA
NM_024093	Homo sapiens hypothetical protein MGC5509 (MGC5509), mRNA
NM_024090	Homo sapiens hypothetical protein MGC5487 (LCE), mRNA
NM_024086	Homo sapiens hypothetical protein MGC3329 (MGC3329), mRNA
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NM_024080	Homo sapiens hypothetical protein MGC2849 (MGC2849), mRNA
NM_024076	Homo sapiens hypothetical protein MGC2628 (MGC2628), mRNA
NM_024074	Homo sapiens hypothetical protein MGC3169 (MGC3169), mRNA
NM_024071	Homo sapiens hypothetical protein MGC2550 (MGC2550), mRNA
NM_024070	Homo sapiens hypothetical protein MGC2463 (MGC2463), mRNA
NM_024069	Homo sapiens hypothetical protein MGC2749 (MGC2749), mRNA

NM_024068	Homo sapiens hypothetical protein MGC2731 (MGC2731), mRNA
NM_024065	Homo sapiens hypothetical protein MGC3062 (MGC3062), mRNA
NM_024061	Homo sapiens hypothetical protein MGC5521 (MGC5521), mRNA
NM_024058	Homo sapiens hypothetical protein MGC5590 (MGC5590), mRNA
NM_024057	Homo sapiens hypothetical protein MGC5585 (MGC5585), mRNA
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NM_024050	Homo sapiens hypothetical protein MGC2594 (MGC2594), mRNA
NM_024049	Homo sapiens hypothetical protein MGC5566 (MGC5566), mRNA
NM_024048	Homo sapiens hypothetical protein MGC3020 (MGC3020), mRNA
NM_024046	Homo sapiens hypothetical protein MGC8407 (MGC8407), mRNA
NM_024045	Homo sapiens nucleolar protein GU2 (GU2), mRNA
NM_024041	Homo sapiens hypothetical protein MGC3180 (MGC3180), mRNA
NM_024039	Homo sapiens hypothetical protein MGC2488 (MGC2488), mRNA
NM_024038	Homo sapiens hypothetical protein MGC2803 (MGC2803), mRNA
NM_024037	Homo sapiens hypothetical protein MGC2603 (MGC2603), mRNA
NM_024032	Homo sapiens hypothetical protein MGC3130 (MGC3130), mRNA
NM_024031	Homo sapiens hypothetical protein MGC3121 (MGC3121), mRNA
NM_024028	Homo sapiens hypothetical protein MGC3265 (MGC3265), mRNA
NM_024027	Homo sapiens hypothetical protein MGC3279 similar to collectins (MGC3279), mRNA
NM_024025	Homo sapiens hypothetical protein MGC1136 (MGC1136), mRNA
NM_024006	Homo sapiens hypothetical protein IMAGE3455200 (IMAGE3455200), mRNA
NM_015653	Homo sapiens DKFZP566F0546 protein (DKFZP566F0546), mRNA
NM_015147	Homo sapiens KIAA0582 protein (KIAA0582), mRNA
NM_016481	Homo sapiens hypothetical protein (HSPC219), mRNA
NM_023940	Homo sapiens hypothetical protein MGC2827 (MGC2827), mRNA
NM_023938	Homo sapiens hypothetical protein MGC2742 (MGC2742), mRNA
NM_023931	Homo sapiens hypothetical protein MGC2474 (MGC2474), mRNA
NM_015517	Homo sapiens MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein (MIZF), mRNA
NM_015540	Homo sapiens DKFZP727M111 protein (DKFZP727M111), mRNA
NM_015043	Homo sapiens KIAA0676 protein (KIAA0676), mRNA
NM_023934	Homo sapiens hypothetical protein MGC2495 (MGC2495), mRNA
NM_023928	Homo sapiens hypothetical protein FLJ12389 similar to acetoacetyl-CoA synthetase (FLJ12389), mRNA
NM_023926	Homo sapiens hypothetical protein FLJ12895 (FLJ12895), mRNA
NM_023924	Homo sapiens hypothetical protein FLJ13441 (FLJ13441), mRNA
NM_020239	Homo sapiens small protein effector 1 of Cdc42 (SPEC1), mRNA
NM_012069	Homo sapiens ATPase, (Na+)/K+ transporting, beta 4 polypeptide (ATP1B4), mRNA
NM_023112	Homo sapiens hypothetical protein FLJ21916 (FLJ21916), mRNA
NM_015324	Homo sapiens KIAA0409 protein (KIAA0409), mRNA
NM_023079	Homo sapiens hypothetical protein FLJ13855 (FLJ13855), mRNA
NM_023077	Homo sapiens hypothetical protein FLJ12439 (FLJ12439), mRNA
NM_023075	Homo sapiens hypothetical protein FLJ11585 (FLJ11585), mRNA
NM_023074	Homo sapiens hypothetical protein FLJ12644 (FLJ12644), mRNA
NM_023073	Homo sapiens hypothetical protein FLJ13231 (FLJ13231), mRNA
NM_023071	Homo sapiens hypothetical protein FLJ13117 (FLJ13117), mRNA
NM_012319	Homo sapiens LIV-1 protein, estrogen regulated (LIV-1), mRNA
NM_023012	Homo sapiens hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4 (FLJ11021), mRNA
NM_023008	Homo sapiens hypothetical protein FLJ12949 (FLJ12949), mRNA

NM_023007	Homo sapiens hypothetical protein FLJ12517 (FLJ12517), mRNA
NM_022918	Homo sapiens hypothetical protein FLJ22104 (FLJ22104), mRNA
NM_022914	Homo sapiens hypothetical protein 24432 (24432), mRNA
NM_022912	Homo sapiens hypothetical protein FLJ13110 (FLJ13110), mRNA
NM_022907	Homo sapiens hypothetical protein FLJ23053 (FLJ23053), mRNA
NM_022905	Homo sapiens hypothetical protein FLJ12572 (FLJ12572), mRNA
NM_022901	Homo sapiens hypothetical protein FLJ21302 (FLJ21302), mRNA
NM_022898	Homo sapiens B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B), mRNA
NM_022841	Homo sapiens hypothetical protein FLJ12994 (FLJ12994), mRNA
NM_022840	Homo sapiens hypothetical protein FLJ23017 (FLJ23017), mRNA
NM_022834	Homo sapiens hypothetical protein FLJ22215 (FLJ22215), mRNA
NM_022832	Homo sapiens hypothetical protein FLJ12552 (FLJ12552), mRNA
NM_022827	Homo sapiens hypothetical protein FLJ21347 (FLJ21347), mRNA
NM_022826	Homo sapiens axotrophin (AXOT), mRNA
NM_022823	Homo sapiens hypothetical protein FLJ22362 (FLJ22362), mRNA
NM_022781	Homo sapiens hypothetical protein FLJ21343 (FLJ21343), mRNA
NM_022780	Homo sapiens hypothetical protein FLJ13910 (FLJ13910), mRNA
NM_022778	Homo sapiens hypothetical protein DKFZp434L0117 (DKFZP434L0117), mRNA
NM_022777	Homo sapiens hypothetical protein FLJ14117 (FLJ14117), mRNA
NM_022771	Homo sapiens hypothetical protein FLJ12085 (FLJ12085), mRNA
NM_022770	Homo sapiens hypothetical protein FLJ13912 (FLJ13912), mRNA
NM_022769	Homo sapiens hypothetical protein FLJ21868 (FLJ21868), mRNA
NM_022767	Homo sapiens hypothetical protein FLJ12484 (FLJ12484), mRNA
NM_022766	Homo sapiens hypothetical protein FLJ23239 (FLJ23239), mRNA
NM_022763	Homo sapiens hypothetical protein FLJ23399 (FLJ23399), mRNA
NM_022762	Homo sapiens hypothetical protein FLJ22318 (FLJ22318), mRNA
NM_022759	Homo sapiens hypothetical protein FLJ21865 (FLJ21865), mRNA
NM_022754	Homo sapiens hypothetical protein FLJ12876 (FLJ12876), mRNA
NM_022752	Homo sapiens hypothetical protein FLJ22059 (FLJ22059), mRNA
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NM_022750	Homo sapiens hypothetical protein FLJ22693 (FLJ22693), mRNA
NM_022747	Homo sapiens hypothetical protein FLJ22558 (FLJ22558), mRNA
NM_022744	Homo sapiens hypothetical protein FLJ13868 (FLJ13868), mRNA
NM_022743	Homo sapiens hypothetical protein FLJ21080 (FLJ21080), mRNA
NM_022741	Homo sapiens hypothetical protein FLJ11850 (FLJ11850), mRNA
NM_022736	Homo sapiens hypothetical protein FLJ14153 (FLJ14153), mRNA
NM_022734	Homo sapiens hypothetical protein FLJ20859 (FLJ20859), mRNA
NM_022731	Homo sapiens similar to rat nuclear ubiquitous casein kinase 2 (NUCKS), mRNA
NM_022727	Homo sapiens HpaII tiny fragments locus 9C (HTF9C), mRNA
NM_012197	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
NM_015136	Homo sapiens KIAA0246 protein (stab1), mRNA
NM_022659	Homo sapiens likely ortholog of mouse early B-cell factor 2 (FLJ11500), mRNA
NM_022571	Homo sapiens putative leukocyte platelet-activating factor receptor (HUMNPIIY20), mRNA
NM_021024	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17-like 1 (HMG17L1), mRNA
NM_019884	Homo sapiens glycogen synthase kinase 3 alpha (GSK3A), mRNA
NM_021034	Homo sapiens interferon induced transmembrane protein 3 (1-8U) (IFITM3),

	mRNA
NM_022445	Homo sapiens thiamin pyrophosphokinase 1 (TPK1), mRNA
NM_022495	Homo sapiens hypothetical protein FLJ12799 (FLJ12799), mRNA
NM_022494	Homo sapiens hypothetical protein FLJ21952 (FLJ21952), mRNA
NM_022492	Homo sapiens hypothetical protein FLJ12788 (FLJ12788), mRNA
NM_022488	Homo sapiens PC3-96 protein (PC3-96), mRNA
NM_022480	Homo sapiens hypothetical protein FLJ12587 (FLJ12587), mRNA
NM_022474	Homo sapiens hypothetical protein FLJ12615 similar to membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 5) (FLJ12615), mRNA
NM_022455	Homo sapiens androgen receptor-associated coregulator 267 (ARA267), mRNA
NM_022452	Homo sapiens hypothetical protein FLJ11618 (FLJ11618), mRNA
NM_022448	Homo sapiens hypothetical protein FLJ21817 similar to Rhoip2 (FLJ21817), mRNA
NM_022373	Homo sapiens hypothetical protein FLJ22313 (FLJ22313), mRNA
NM_022370	Homo sapiens hypothetical protein FLJ21044 similar to Rbig1 (FLJ21044), mRNA
NM_022368	Homo sapiens praja 1 (PJA1), mRNA
NM_022366	Homo sapiens hypothetical protein FLJ23182 (FLJ23182), mRNA
NM_022361	Homo sapiens popeye protein 3 (POP3), mRNA
NM_022360	Homo sapiens human epididymis-specific 3 beta (HE3-BETA), mRNA
NM_022342	Homo sapiens kinesin family member 9 (KIF9), mRNA
NM_022372	Homo sapiens G protein beta subunit-like (GBL), mRNA
NM_022158	Homo sapiens fructosamine-3-kinase (FN3K), mRNA
NM_022137	Homo sapiens secreted modular calcium-binding protein 1 (SMOC1), mRNA
NM_022118	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
NM_022116	Homo sapiens fidgetin-like 1 (FIGNL1), mRNA
NM_022103	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
NM_022070	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
NM_022065	Homo sapiens hypothetical protein FLJ21877 (FLJ21877), mRNA
NM_021970	Homo sapiens mitogen-activated protein kinase kinase 1 interacting protein 1 (MAP2K1IP1), mRNA
NM_019081	Homo sapiens KIAA0430 gene product (KIAA0430), mRNA
NM_021981	Homo sapiens pre-T/NK cell associated protein (1D12A), mRNA
NM_020121	Homo sapiens UDP-glucose ceramide glucosyltransferase-like 2 (UGCGL2), mRNA
NM_006683	Homo sapiens human epididymis-specific 3 alpha (HE3-ALPHA), mRNA
NM_006077	Homo sapiens calcium binding atopy-related autoantigen 1 (CBARA1), mRNA
NM_021934	Homo sapiens hypothetical protein FLJ11773 (FLJ11773), mRNA
NM_021933	Homo sapiens hypothetical protein FLJ12438 (FLJ12438), mRNA
NM_021930	Homo sapiens Rad50-interacting protein 1 (FLJ11785), mRNA
NM_021929	Homo sapiens hypothetical protein FLJ21613 similar to rat corneal wound healing related protein (FLJ21613), mRNA
NM_007272	Homo sapiens chymotrypsin C (caldecrin) (CTRC), mRNA
NM_004237	Homo sapiens thyroid hormone receptor interactor 13 (TRIP13), mRNA
NM_003849	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
NM_021648	Homo sapiens KIAA0721 protein (KIAA0721), mRNA
NM_021831	Homo sapiens hypothetical protein FLJ21839 (FLJ21839), mRNA
NM_021827	Homo sapiens hypothetical protein FLJ23514 (FLJ23514), mRNA
NM_021195	Homo sapiens claudin 6 (CLDN6), mRNA
NM_018947	Homo sapiens cytochrome c (HCS), mRNA

NM_021732	Homo sapiens hypothetical protein PP5395 (PP5395), mRNA
NM_021730	Homo sapiens hypothetical protein PP1044 (PP1044), mRNA
NM_021643	Homo sapiens GS3955 protein (GS3955), mRNA
NM_015180	Homo sapiens synaptic nuclei expressed gene 2 (SYNE-2), mRNA
NM_021633	Homo sapiens kelch-like protein C3IP1 (C3IP1), mRNA
NM_021629	Homo sapiens guanine nucleotide binding protein beta subunit 4 (GNB4), mRNA
NM_021627	Homo sapiens sentrin-specific protease (SENP2), mRNA
NM_021626	Homo sapiens likely homolog of rat and mouse retinoid-inducible serine carboxypeptidase (RISC), mRNA
NM_021622	Homo sapiens pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 1 (PLEKHA1), mRNA
NM_012408	Homo sapiens protein kinase C binding protein 1 (PRKCBP1), mRNA
NM_021252	Homo sapiens RAB18, member RAS oncogene family (RAB18), mRNA
NM_020806	Homo sapiens gephyrin (GPHN), mRNA
NM_021258	Homo sapiens interleukin 22 receptor (IL22R), mRNA
NM_021235	Homo sapiens epidermal growth factor receptor substrate EPS15R (EPS15R), mRNA
NM_021204	Homo sapiens E-1 enzyme (MASA), mRNA
NM_021191	Homo sapiens neurogenic differentiation 4 (NEUROD4), mRNA
NM_021178	Homo sapiens enhancer of invasion 10 (HEI10), mRNA
NM_021127	Homo sapiens phorbol-12-myristate-13-acetate-induced protein 1 (PMAIP1), mRNA
NM_021114	Homo sapiens serine protease inhibitor, Kazal type, 2 (acrosin-trypsin inhibitor) (SPINK2), mRNA
NM_021103	Homo sapiens thymosin, beta 10 (TMSB10), mRNA
NM_006435	Homo sapiens interferon induced transmembrane protein 2 (1-8D) (IFITM2), mRNA
NM_021073	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
NM_003142	Homo sapiens Sjogren syndrome antigen B (autoantigen La) (SSB), mRNA
NM_003888	Homo sapiens aldehyde dehydrogenase 1 family, member A2 (ALDH1A2), mRNA
NM_013234	Homo sapiens muscle specific gene (M9), mRNA
NM_021067	Homo sapiens KIAA0186 gene product (KIAA0186), mRNA
NM_021020	Homo sapiens leucine zipper, putative tumor suppressor 1 (LZTS1), mRNA
NM_021025	Homo sapiens homeo box 11-like 2 (HOX11L2), mRNA
NM_021003	Homo sapiens protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform (PPM1A), mRNA
NM_020674	Homo sapiens cytochrome P450 monooxygenase (CYP-M), mRNA
NM_019612	Homo sapiens hypothetical protein R30953_1 (R30953_1), mRNA
NM_020904	Homo sapiens pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 4 (PLEKHA4), mRNA
NM_020686	Homo sapiens NPD009 protein (NPD009), mRNA
NM_020684	Homo sapiens NPD007 protein (NPD007), mRNA
NM_020683	Homo sapiens AD026 protein (AD026), mRNA
NM_020679	Homo sapiens AD023 protein (AD023), mRNA
NM_020677	Homo sapiens HSCARG protein (HSCARG), mRNA
NM_020675	Homo sapiens AD024 protein (AD024), mRNA
NM_020673	Homo sapiens RAB22A, member RAS oncogene family (RAB22A), mRNA
NM_020660	Homo sapiens connexin-36 (CX36), mRNA
NM_019108	Homo sapiens hypothetical protein FLJ12886 (FLJ12886), mRNA
NM_018838	Homo sapiens 13kDa differentiation-associated protein (DAP13), mRNA

NM_018434	Homo sapiens goliath protein (GP), mRNA
NM_020437	Homo sapiens similar to aspartate beta hydroxylase (ASPH) (LOC57168), mRNA
NM_020524	Homo sapiens hematopoietic PBX-interacting protein (HPIP), mRNA
NM_018638	Homo sapiens ethanolamine kinase (EKI1), mRNA
NM_016326	Homo sapiens chemokine-like factor 1 (CKLF1), mRNA
NM_016951	Homo sapiens chemokine-like factor 1 (CKLF1), mRNA
NM_020143	Homo sapiens putatative 28 kDa protein (LOC56902), mRNA
NM_020141	Homo sapiens protein x 013 (AD-020), mRNA
NM_020122	Homo sapiens potassium channel modulatory factor (PCMF), mRNA
NM_018843	Homo sapiens mitochondrial carrier family protein (MCFP), mRNA
NM_018840	Homo sapiens putative Rab5-interacting protein (RIP5), mRNA
NM_016303	Homo sapiens pp21 homolog (LOC51186), mRNA
NM_016300	Homo sapiens cyclic AMP-regulated phosphoprotein, 21 kD (ARPP-21), mRNA
NM_016299	Homo sapiens likely ortholog of mouse heat shock protein, 70 kDa 4 (LOC51182), mRNA
NM_013259	Homo sapiens neuronal protein (NP25), mRNA
NM_005064	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 23 (SCYA23), mRNA
NM_013260	Homo sapiens transcriptional regulator protein (HCNGP), mRNA
NM_020433	Homo sapiens hypothetical protein LOC57158 (LOC57158), mRNA
NM_020410	Homo sapiens CGI-152 protein (CGI-152), mRNA
NM_020401	Homo sapiens nuclear pore complex protein (NUP107), mRNA
NM_020400	Homo sapiens G protein-coupled receptor 92 (GPR92), mRNA
NM_020397	Homo sapiens CamKI-like protein kinase (LOC57118), mRNA
NM_020388	Homo sapiens CATX-15 protein (CATX-15), mRNA
NM_020386	Homo sapiens HRAS-like suppressor (HRASLS), mRNA
NM_020361	Homo sapiens carboxypeptidase B precursor (CPAH), mRNA
NM_020357	Homo sapiens PEST-containing nuclear protein (pcnp), mRNA
NM_020345	Homo sapiens I-kappa-B-interacting Ras-like protein 1 (KBRAS1), mRNA
NM_020360	Homo sapiens phospholipid scramblase 3 (PLSCR3), mRNA
NM_020348	Homo sapiens cyclin M1 (CNNM1), mRNA
NM_000888	Homo sapiens integrin, beta 6 (ITGB6), mRNA
NM_020181	Homo sapiens myelin proteolipid protein-like protein (PLPL), mRNA
NM_020144	Homo sapiens poly(A) polymerase beta (testis specific) (PAPOLB), mRNA
NM_020202	Homo sapiens Nit protein 2 (NIT2), mRNA
NM_020250	Homo sapiens MOST2 protein (MOST2), mRNA
NM_020237	Homo sapiens MOST-1 protein (MOST-1), mRNA
NM_020234	Homo sapiens x 009 protein (MDS009), mRNA
NM_020128	Homo sapiens nuclear protein double minute 1 (MDM1), mRNA
NM_020169	Homo sapiens latexin protein (LXN), mRNA
NM_020133	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta), mRNA
NM_020241	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (SEMA6B), mRNA
NM_020163	Homo sapiens semaphorin sem2 (LOC56920), mRNA
NM_020199	Homo sapiens HTGN29 protein (HTGN29), mRNA
NM_020197	Homo sapiens HSKM-B protein (HSKM-B), mRNA
NM_020200	Homo sapiens HHGP protein (HHGP), mRNA
NM_020195	Homo sapiens HCDI protein (HCDI), mRNA
NM_020198	Homo sapiens GK001 protein (GK001), mRNA
NM_020117	Homo sapiens hypothetical protein FLJ10595 (FLJ10595), mRNA

NM_020119	Homo sapiens hypothetical protein FLB6421 (FLB6421), mRNA
NM_020162	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 33 (DDX33), mRNA
NM_020215	Homo sapiens hypothetical protein DKFZp761F2014 (DKFZp761F2014), mRNA
NM_020221	Homo sapiens hypothetical protein DKFZp547I224 (DKFZp547I224), mRNA
NM_020217	Homo sapiens hypothetical protein DKFZp547I014 (DKFZp547I014), mRNA
NM_020161	Homo sapiens hypothetical protein DKFZp547H025 (DKFZp547H025), mRNA
NM_020186	Homo sapiens DC11 protein (DC11), mRNA
NM_020205	Homo sapiens cellular zinc finger anti-NF-kappaB Cezanne (CEZANNE), mRNA
NM_019887	Homo sapiens second mitochondria-derived activator of caspase (SMAC), mRNA
NM_019892	Homo sapiens phosphatidylinositol (4,5) bisphosphate 5-phosphatase homolog; phosphatidylinositol polyphosphate 5-phosphatase type IV (PPI5PIV), mRNA
NM_019885	Homo sapiens cytochrome P450 retinoid metabolizing protein (P450RAI-2), mRNA
NM_019845	Homo sapiens candidate mediator of the p53-dependent G2 arrest (REPRIMO), mRNA
NM_019853	Homo sapiens protein phosphatase 4 regulatory subunit 2 (PPP4R2), mRNA
NM_013301	Homo sapiens protein predicted by clone 23882 (HSU79303), mRNA
NM_013300	Homo sapiens protein predicted by clone 23733 (HSU79274), mRNA
NM_013296	Homo sapiens LGN protein (HSU54999), mRNA
NM_013293	Homo sapiens transformer-2 alpha (htra-2 alpha) (HSU53209), mRNA
NM_013310	Homo sapiens hypothetical protein (AF038169), mRNA
NM_018975	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1), mRNA
NM_019082	Homo sapiens putative nucleolar RNA helicase (NOH61), mRNA
NM_019020	Homo sapiens hypothetical protein (FLJ20748), mRNA
NM_019058	Homo sapiens HIF-1 responsive RTP801 (FLJ20500), mRNA
NM_019056	Homo sapiens neuronal protein 17.3 (P17.3), mRNA
NM_019042	Homo sapiens hypothetical protein (FLJ20485), mRNA
NM_019061	Homo sapiens phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit (3-PAP), mRNA
NM_018986	Homo sapiens hypothetical protein (FLJ20356), mRNA
NM_019034	Homo sapiens ras homolog gene family, member F (in filopodia) (ARHF), mRNA
NM_019062	Homo sapiens hypothetical protein (FLJ20225), mRNA
NM_019038	Homo sapiens hypothetical protein (FLJ11045), mRNA
NM_019044	Homo sapiens hypothetical protein (FLJ10996), mRNA
NM_018180	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 32 (DDX32), mRNA
NM_019028	Homo sapiens hypothetical protein similar to ankyrin repeat-containing priotein AKR1 (FLJ10852), mRNA
NM_019014	Homo sapiens similar to DNA-directed RNA polymerase I (135 kDa) (Rpo1-2), mRNA
NM_019023	Homo sapiens hypothetical protein (FLJ10640), mRNA
NM_018162	Homo sapiens hypothetical protein FLJ10633 (FLJ10633), mRNA
NM_019067	Homo sapiens hypothetical protein (FLJ10613), mRNA
NM_019057	Homo sapiens hypothetical protein (FLJ10404), mRNA
NM_018846	Homo sapiens SBBI26 protein (SBBI26), mRNA
NM_016483	Homo sapiens hypothetical protein (HSPC226), mRNA
NM_018400	Homo sapiens voltage-gated sodium channel beta-3 subunit (scn3b gene)

	(HSA243396), mRNA
NM_018700	Homo sapiens tripartite motif-containing 36 (TRIM36), mRNA
NM_018547	Homo sapiens hypothetical protein PRO2964 (PRO2964), mRNA
NM_018546	Homo sapiens hypothetical protein PRO2958 (PRO2958), mRNA
NM_018544	Homo sapiens hypothetical protein PRO2949 (PRO2949), mRNA
NM_018634	Homo sapiens hypothetical protein PRO2893 (PRO2893), mRNA
NM_018543	Homo sapiens hypothetical protein PRO2859 (PRO2859), mRNA
NM_018542	Homo sapiens hypothetical protein PRO2834 (PRO2834), mRNA
NM_018538	Homo sapiens erythroblast membrane-associated protein (ERMAP), mRNA
NM_018534	Homo sapiens hypothetical protein PRO2714 (PRO2714), mRNA
NM_018530	Homo sapiens hypothetical protein PRO2521 (PRO2521), mRNA
NM_018627	Homo sapiens hypothetical protein PRO2405 (PRO2405), mRNA
NM_018523	Homo sapiens hypothetical protein PRO2325 (PRO2325), mRNA
NM_018519	Homo sapiens hypothetical protein PRO2266 (PRO2266), mRNA
NM_018517	Homo sapiens hypothetical protein PRO2214 (PRO2214), mRNA
NM_018621	Homo sapiens hypothetical protein PRO2198 (PRO2198), mRNA
NM_018619	Homo sapiens hypothetical protein PRO2133 (PRO2133), mRNA
NM_018618	Homo sapiens hypothetical protein PRO2121 (PRO2121), mRNA
NM_018616	Homo sapiens hypothetical protein PRO2037 (PRO2037), mRNA
NM_018512	Homo sapiens hypothetical protein PRO2015 (PRO2015), mRNA
NM_018610	Homo sapiens hypothetical protein PRO1942 (PRO1942), mRNA
NM_018510	Homo sapiens hypothetical protein PRO1866 (PRO1866), mRNA
NM_018507	Homo sapiens hypothetical protein PRO1843 (PRO1843), mRNA
NM_018606	Homo sapiens hypothetical protein PRO1787 (PRO1787), mRNA
NM_018589	Homo sapiens hypothetical protein PRO1635 (PRO1635), mRNA
NM_018587	Homo sapiens hypothetical protein PRO1617 (PRO1617), mRNA
NM_018503	Homo sapiens hypothetical protein PRO1598 (PRO1598), mRNA
NM_018586	Homo sapiens hypothetical protein PRO1584 (PRO1584), mRNA
NM_018502	Homo sapiens hypothetical protein PRO1580 (PRO1580), mRNA
NM_018603	Homo sapiens hypothetical protein PRO1496 (PRO1496), mRNA
NM_018584	Homo sapiens hypothetical protein PRO1489 (PRO1489), mRNA
NM_018582	Homo sapiens hypothetical protein PRO1483 (PRO1483), mRNA
NM_018602	Homo sapiens DnaJ (Hsp40) homolog, subfamily A, member 4 (DNAJA4), mRNA
NM_018578	Homo sapiens hypothetical protein PRO1257 (PRO1257), mRNA
NM_018576	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
NM_018497	Homo sapiens hypothetical protein PRO1048 (PRO1048), mRNA
NM_018565	Homo sapiens hypothetical protein PRO0899 (PRO0899), mRNA
NM_018562	Homo sapiens hypothetical protein PRO0386 (PRO0386), mRNA
NM_018590	Homo sapiens hypothetical protein PRO0082 (PRO0082), mRNA
NM_018667	Homo sapiens sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) (SMPD3), mRNA
NM_017544	Homo sapiens transcription factor NRF (NRF), mRNA
NM_018468	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS033 (MDS033), mRNA
NM_018467	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS032 (MDS032), mRNA
NM_018464	Homo sapiens uncharacterized hematopoietic stem/progenitor cells protein MDS029 (MDS029), mRNA
NM_018688	Homo sapiens bridging integrator 3 (BIN3), mRNA
NM_018686	Homo sapiens CMP-N-acetylneuraminic acid synthase (CMAS), mRNA
NM_018446	Homo sapiens glycosyltransferase AD-017 (AD-017), mRNA

NM_018416	Homo sapiens FOXJ2 forkhead factor (FHX), mRNA
NM_018407	Homo sapiens putative integral membrane transporter (LC27), mRNA
NM_018472	Homo sapiens uncharacterized hypothalamus protein HT011 (HT011), mRNA
NM_018471	Homo sapiens uncharacterized hypothalamus protein HT010 (HT010), mRNA
NM_018470	Homo sapiens uncharacterized hypothalamus protein HT009 (HT009), mRNA
NM_018469	Homo sapiens uncharacterized hypothalamus protein HT008 (HT008), mRNA
NM_017523	Homo sapiens XIAP associated factor-1 (HSXIAPAF1), mRNA
NM_017514	Homo sapiens SEX gene (HSSEXGENE), mRNA
NM_017512	Homo sapiens rTS beta protein (HSRTSBETA), mRNA
NM_016536	Homo sapiens HSPC059 protein (HSPC059), mRNA
NM_018553	Homo sapiens ELG protein (HSA277841), mRNA
NM_018403	Homo sapiens transcription factor (SMIF gene) (HSA275986), mRNA
NM_018404	Homo sapiens centaurin, alpha 2 (CENTA2), mRNA
NM_018401	Homo sapiens gene for serine/threonine protein kinase (HSA250839), mRNA
NM_017582	Homo sapiens NICE-5 protein (HSA243666), mRNA
NM_018684	Homo sapiens hepatocellular carcinoma-associated antigen 127 (HCA127), mRNA
NM_018477	Homo sapiens uncharacterized hypothalamus protein HARP11 (HARP11), mRNA
NM_018652	Homo sapiens golgin-like protein (GLP), mRNA
NM_017962	Homo sapiens hypothetical protein FLJ20825 (FLJ20825), mRNA
NM_017961	Homo sapiens hypothetical protein FLJ20813 (FLJ20813), mRNA
NM_017960	Homo sapiens hypothetical protein FLJ20808 (FLJ20808), mRNA
NM_017959	Homo sapiens hypothetical protein FLJ20802 (FLJ20802), mRNA
NM_017958	Homo sapiens hypothetical protein FLJ20783 (FLJ20783), mRNA
NM_017957	Homo sapiens epsin 3 (FLJ20778), mRNA
NM_017956	Homo sapiens hypothetical protein FLJ20772 (FLJ20772), mRNA
NM_017950	Homo sapiens hypothetical protein FLJ20753 (FLJ20753), mRNA
NM_017949	Homo sapiens hypothetical protein FLJ20739 (FLJ20739), mRNA
NM_017946	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
NM_017953	Homo sapiens hypothetical protein FLJ20729 (FLJ20729), mRNA
NM_017943	Homo sapiens hypothetical protein FLJ20725 (FLJ20725), mRNA
NM_017941	Homo sapiens hypothetical protein FLJ20721 (FLJ20721), mRNA
NM_017938	Homo sapiens hypothetical protein FLJ20716 (FLJ20716), mRNA
NM_017937	Homo sapiens hypothetical protein FLJ20712 (FLJ20712), mRNA
NM_017932	Homo sapiens hypothetical protein FLJ20700 (FLJ20700), mRNA
NM_017929	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
NM_017928	Homo sapiens hypothetical protein FLJ20694 (FLJ20694), mRNA
NM_017925	Homo sapiens hypothetical protein FLJ20686 (FLJ20686), mRNA
NM_017920	Homo sapiens hypothetical protein FLJ20654 (FLJ20654), mRNA
NM_017919	Homo sapiens hypothetical protein FLJ20651 (FLJ20651), mRNA
NM_017918	Homo sapiens hypothetical protein FLJ20647 (FLJ20647), mRNA
NM_017917	Homo sapiens hypothetical protein FLJ20644 (FLJ20644), mRNA
NM_017916	Homo sapiens hypothetical protein FLJ20643 (FLJ20643), mRNA
NM_017915	Homo sapiens hypothetical protein FLJ20641 (FLJ20641), mRNA
NM_017912	Homo sapiens hypothetical protein FLJ20637 (FLJ20637), mRNA
NM_017909	Homo sapiens hypothetical protein FLJ20627 (FLJ20627), mRNA
NM_017907	Homo sapiens hypothetical protein FLJ20625 (FLJ20625), mRNA
NM_017903	Homo sapiens hypothetical protein FLJ20618 (FLJ20618), mRNA
NM_017901	Homo sapiens two-pore channel 1, homolog (KIAA1169), mRNA
NM_017900	Homo sapiens hypothetical protein FLJ20608 (FLJ20608), mRNA
NM_017899	Homo sapiens hypothetical protein FLJ20607 (TSC), mRNA